AL844183 Mouse DNA

AC134836 Mus muscu AC144720 Apis mell AC144421 Rattus no AL645625 Mouse DNA AC139439 Rattus no AC104229 Homo sapi AC13255 Rattus no AX664499 Sequence U13369 Homo sapi AC13959 Rattus no AC13939 Rattus no AC139510 Rattus no BX545908 Homo sapi AC139510 Rattus no AC149255 Papio anu AC169586 Mus muscu AC169586 Mus muscu AC169586 Mus muscu AC169586 Mus muscu AC169586 Mus muscu

AC009785 Homo sapi AC087227 Mus muscu AC114008 Mus muscu AC079422 Mus muscu

Homo sapi Homo sapi

AL590990

PAT 24-JAN-2001

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Gaps

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Hayden,M.R. and Kastelein,J.J.
Lpl variant therapeutics
Datent: WO 0100220-A 4 04-JAN-2001;
THE UNIVERSITY OF BRITISH COLUMBIA (CA); Amsterdam Molecular
Therapeutics B.V. (AMT) (NL); Academic Hospital at the University
of Amsterdam (NL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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100.0%; Pred. No. 1.1e-278;
iive 0; Mismatches 0;
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/db_xref="taxon:9606"
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1. .2565
/organism="Homo sapiens"
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AC144421
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BX545908
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AL645762
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AC149255
AC105986
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AL590990
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AC087226 Mus muscu
AC116720 Mus muscu
AL61432 Homo sapi
Continuation (4 of
AC069368 Homo sapi
AC064799 Mus muscu
AC073957 Homo sapi
AC073957 Homo sapi
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 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                      4526729 segs, 23644849745 residues
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Maximum Match 100*
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Database :

Result No.

Seguence:

Run on:

Searched:

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AC103691 82781 bp DNA linear PRI 01-MAY-2002
Homo sapiens chromosome 15, clone RP11-959H21, complete sequence.
AC103691
                                                                                                                                                                                                                                                                                                                                  1110 AAAAAGGGCAACAAAGGGGAAGGGCCAAAAGCACCCCCAACGAAAAGACAGGGACAGAA 1169
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Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 82781)
1516 GAGGCCCCAAACACCAAAGCCCAAGAAACAGAAAAGCCCGCGGCACGAACAGACACACACAC 1575
                                                                PAT 28-DEC-1997
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                                                                                                                                                                                                                                                 Length 7218;
                                                                                                                   Unclassified.

1 (bases 1 to 7218)

Dorner,F., Scheiflinger,F. and Falkner,F.Gunter. Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997;

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lander, E
                                                                                                                                                                                            Query Match 9.6%; Score 129.6; DB 6; Best Local Similarity 1.6%; Pred. No. 1.4e-17; Matches 6; Conservative 289; Mismatches 83;
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                                                               7218 bp Sequence 14 from patent US 5670367.
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                                                                                                                                                          1. .7218
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/mol_type="unassigned
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                  1321 AGCAGAGAAGAGAGACCCCGC
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organism="Homo sapiens"

/mol\_type="genomic\_DN /db\_xref="taxon:9606"

/chromosome="15"

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137. . . 883 'rpt\_family="L1PA9"

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frpt_family="L2"
437. .883
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/rpt_family="L2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (U-MAY-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 1, 2002 this sequence version replaced gi:17149576. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Only the first 82.8 kilobases of this clone are being submitted.
The remainder overlaps accession number AC013553 [WICGR project
L2203].
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         Homo sapiens chromosome 15, clone RP11-959H21
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complement (2504. .2809)
/rpt\_family="AluSx"
complement (2884. .3005)
/rpt\_family="MIR" rpt\_family="MER81" /rpc\_family="Alusx" 5559. rpt\_family="AT\_rich" 408. .3576 9954. .1024P 'rpt family="(TAGA)n" /rpt\_family="L1MC3"
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24965 GAAGAAGGAGGAGGAAGAA-GAAGGAAGAACTAAGAAGGAAGAAAGAAGAAAGAAAG 24907
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 188507)
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                                                                                                                                         AGAAAAGCAGGAGACCAGAAAAAGGGACCGCAGGAGAAAAGGCCAGCAAAAAGGAAAAG
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Mus musculus chromosome 3, clone RP23-474P24
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1298 CGCGGCACGAACAGACCACACACAGCAGAGAGAGAAG
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Mus musculus chromosome 3, clone
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Pred. No. 4.2e-12;
0; Mismatches 604; Indels 5
                                                                                                                                    /rpt_family="MIR3"
complement(13342. .13480)
/rpt_family="Limb"
13638. .13949
          complement (11055. .11349)
/rpt family="Alux"
complement (11362. .11654)
/rpt family="Aludb"
complement (11655. .11876)
/rpt family="Aludb"
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2593. .....
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/rpt_family="LIME4A"
14254. .14475
/rpt_family="L2"
14921. .14997
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/rpt_family="MER47A"
16220. 1624
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/rpt_family="Alusx"
/9455. 19627
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rpt family="MER47A"
7177. .17313
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/rpt_family="MER5B"
20707. .20828
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complement(16248. ...
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8301. .18391
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/rpt family="L1"

18859. 19157

/rpt family="L1"

19158. 19454
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complement(12727.
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Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
                                                                                                                 Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project_Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="RPCI-23 Female Mouse BAC"
1. .11149
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16699. 16747
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complement(17224. 17358)
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/rpt_f-
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complement (430. .1594)
/rpt family="Lx9"
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206. .5227
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                                                                                                                                                                                                              Center project name: L22816
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7500. 7535
/rpt_family="(ATGGTG)n"
8932. .9028
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2189. .2847
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12002. .12056
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11150..11155
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Ginde, S., Gord, S., Goyette, M., Gage, D., Galagan, J., Gardyna, S., Hagos, B., Horton, L., Hulme, W., Iliev, L., Grand-Pierre, N., Kamat, A., Kartaras, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lindlad-Toh, K., Liu, G., MacLean, C., Macdonald, D., Major, J., Marquis, N., Matthews, C., Macdorald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Minora, T., Mlenga, V., Murphy, T., Naylor, J., Naylor, C., Nicol, R., Norbu, C., Retra, R., Friback, M., Riley, R., Rise, C., Rogov, P., Raymond, C., Retra, R., Kiback, M., Riley, R., Rise, C., Rogov, R., Sewan, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schuback, R., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Viel, R., Vo, A., Wilson, M., Trayis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., W., Wilson, D., Ye, W.J., Young, G., Direct Submission
L. Submitten, J., Zembek, L., Zimmer, A. and Zody, M., Ye, W.J., Young, G., Submission
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Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 188507)

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3 Shiren, B., Musbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Colymore, A., Cooke, P., Coruw, B., DeArellann, K., Cook, A., Cook, P., Coruw, B., DeArellann, K., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, D., Kamat, A., Katls, C., Landers, T., Levine, R., Jones, C., Lindblad-Toh, K., Liu, G., Lui, X., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Matthews, C., McCartby, M., Maldran, J., Meneus, L., Mihova, T., Mengay, T., Naylor, J., Nguyen, C., Nicol, R., Mihova, T., Mengay, V., Mihova, T., Ohomeall, P., O'Neil, D., Peterson, K., Peterson, K., Peterson, K., Schauer, S., Schubeack, R., Searen, P., Severy, P., Spencer, B., Stange-Thomann, M., Stojanovic, N., Stubbs, M., Vassills, M., Venkataraman, V. S., Viel, R., Travers, M., Vassills, M., Venkataraman, V.S., Viel, R., Zimmer, A. and Zody, M., Direct, M., Solmish, M., Simmer, A. and Zody, M., Shahatter, M., Submish, M., Samhon, J., Zembek, L., Zimmer, A. and Zody, M., Shahatter, M., Submish, M., Simher, J., Zimmer, A., and Zody, M., Shahatter, M., Submish, M., Schmish, J., Zimmer, A. and Zody, M., Shahatter, M., Shahatter, M., Simher, M., Simher, M., Shahatter, M., Shahatter, M., Samhatter, M., Shahatter, M., Shahatre, M., Shahatre, M., Samhatter, M., Shahatre, M., Samhatre, M., Shahatre, M., Samhatre, M., Shahatre, M., Samhatre, M., Shahatter, M., Shahatre, M., Samhatre, M., Shahatre, M., Samhatre, M., Shahatre, M., Samhatre, M., Shahatre, M., Samhatre, M.,
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Birren,B., Musbaum,C., Lander,B., Abouelleil,A., Allen,N., Anderson,M., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T., Cook,A., Cook,P., Corum,B., Dehrellano,K., Diaz,J.S., Dodge,S., Corum,B., Dehrellano,K., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S., Graham,L., Grand-Pierre,N., Hafez,N., Hagoplan,J., Gardyna,S., Hall,J., Hulme,W., Iliev,I., Vohnson,R., Jones,C., Lindblad-Toh,K., Liu,X., Lul,A., Madpulan,D., Hagos,B., Madonald,P., Major,J., Manders,T., Levine,R., Madonald,P., Major,J., Manders,T., Levine,R., Madonald,P., Major,J., Manneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Naple,C., Nacch,R., Norbu,C., O'Connor,T., O'Donnell,P., O'Neil,D., Olliver,J., Peterson,K., Phunkhang,P., Pierre,N., Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P., Roman,J., Schauber,S., Schupback,R., Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N., Schauback,R., Travers,M., Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X., Wman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
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All repeats were identified using RepeatMasker:
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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vigna.

vigna.

i (bases 1 to 10732)

ITLE

Gene encoding cellulose synthesizer

JURNAL

PATENTIAN

OURNAL

PATENTIAN

OS Vigna angularis

PN 29-FEB-2000;

PR 26-AUG-1998 JP 1998239998

PR XOICHI MIZUNO, TOMONIKO KATO, SHIGERU SATO, DAISUKE SHIBATA PC

CLANIS/09, AO1HS/00, COTKI6/40, CLIZNIS/10, CLIZNIS/102/7 PC

CLIZNIS/09, CLIZNIS/10, CLIZNIS/10, CLIZNIS/10, CLIZNIS/100, PC

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CLIZNIS/00, CLIZNIS/10, CLIZNIS/10, CLIZNIS/10, CLIZNIS/10, CLIZNIS/100, PC

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JP 2000060568-A/1.
Vigna angularis (adzuki bean)
Vigna angularis
Vigna angularis
Spermatophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; core eudicots; cosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                CACCGCGGAGGAAAGCCAGACAAGCGAAAAGAAGCAGGCGAAACGGGCGAACACAGAAC
                                                                                                                                                                                                                                                                                                                                                                                                C12NS/00, (C12N15/00, C12R1:91), (C12NS/00, C12R1:91)
Location/Qualifiers
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    10732
    /organism="Vigna angularis"
/mol_type="genomic DNA"
    /db_xref="taxon:3914"

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                                           17362. .17395

/rpt_family="(TTTG)n"

complement(17404. .17491)

/rpt_family="B1_MM"

complement(17415. .17516)

/rpt_family="B4A"
                                                                                                                                                                                                                                           rpt_family="L1MC4"
8327. :18392
rpt_family="L1MC4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rpt_family="CT-rich"
omplement(22968. .23114)
rpt_family="B1_MM"
                                                                                                                                                                                                                                                                                                                                        rpt_family="(TCTA)n"
9720. .19742
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2266. .22334
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rpt family="(TTTA)n"
1970. .22017
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24715. .24755
/rpt_family="(CA)n"
24755. .24825
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                                                                                                                                                                                     rpt_family="B1_MM"
8097. .18215
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8400. .18430
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family="(A)n"
                         family="B1_MM"
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complement(18216
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                             GACAAGAGAGAACCAGACCCAAGGGGGGGGGGGCGCAGGGCCAGGAGCAACCCAGGCC
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                   Gaps
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                   12;
    Length 10732;
               Conservative 522; Mismatches 611; Indels
7.7%; Score 103; DB 6;
15.3%; Pred. No. 7.4e-12;
        15.3%;
        Local Similarity
             207;
Query Match
Best Local S:
Matches 207,
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1193 AGCGCAGAGAAAAAAGGCCCCAAGGCGAAGGCCAAAGCAAAGGAGAACCCCAAAGGAACG 1252
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Mus musculus chromosome 16 clone RP23-103M13, WORKING DRAFT SEQUENCE, 72 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Consensus quality: 151438 bases at least Q40
Consensus quality: 173959 bases at least Q30
Consensus quality: 173959 bases at least Q30
Consensus quality: 185196 bases at least Q30
Consensus quality: 185196 bases at least Q30
Consensus quality: 185196 bases at least Q30
Estimated insert size: 258885; sum-of-contigs estimation
Quality coverage: 3.77 in Q20 bases; sum-of-contigs estimation
Quality coverage: 3.21 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a "working draft' sequence. It currently
* consists of 72 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOE Joint
94598, USA
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Sciurognathi; Muridae; Murinae; Mus.
                                                    GACCGGACGAGGCCCCAAACACCCAAGGAAACAGAAAAGCCCGCGGGCACGAACAGA
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DOE Joint Genome Institute.
Direct Submission Separation Sequencing Facility,
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA
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unknown length
of 1194 bp in length
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Center clone name: RPCI-23_103M13
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Web site: http://www.jgi.doe.gov
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Unpublished
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Mammalia, Eutheria, Rodentia,
1 (bases 1 to 265985)
DOE Joint Genome Institute.
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Center: Joint Genome Institute
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HTG; HTGS PHASE1; HTGS DRAFT.
Mus musculus (house mouse)
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48753: contig of 1473 48853: gap of unknown 50036: contig of 1183 51016: gap of unknown 51270: contig of 1184 51370: gap of unknown 52534: contig of 1164 52634: gap of unknown 53751: contig of 1117 53851: gap of unknown 54995: contig of 1148 55095: gap of unknown	contiggap of gap of gap of gap of gap of contiggap of contiggap of contiggap of gap of contiggap	126383 /organism="Mus musculus" /or_type="genomic DNA" /db_xref="taxon:10090" /chromosome="16"
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	FEATURES	source
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aknown f 1197 nknown f 1210 nknown f 1110 f 1110 f 1125 f 1125 f 1134 f 1134 f 1134	contig of 1130 bp in length rap of unknown length contrag of 1164 bp in length contrag of 1165 bp in length sap of unknown length app of unknown length app of unknown length contrag of 1135 bp in length app of unknown length langth contrag of 1135 bp in length app of unknown length length contrag of 1135 bp in length app of unknown length length app in length app of unknown length app	of unknown length ig of 1134 bp in of unknown length ig of 1150 bp in of unknown length
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 267182)
                         musculus (house mouse)
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                                                                                                                                                                                                                                                                        596 AAAGAACCGCGAACAACAACGGCAGAGACAAAAAGCAGAGAGAGAGAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             656 CGAAGACCGCCAGAGCCCACAAAGCCCAACAAGAAAGACACGGGAGAGAAACCCA
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                                                                                                                                                      Length 265985;
                                                                                                                                                                                                                        Indels
/clone="RP23-103M13"
/clone_lib="RPCI mouse BAC library 23"
                                                                                                                                Ouery Match 7.6%; Score 102.2; DB 2; Best Local Similarity 46.8%; Pred. No. 9.7e-12; Matches 374; Conservative 0; Mismatches 422;
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AC116720 -AC116720.4 GI:30018035 HTG; HTGS\_PHASE1; HTGS\_DRAFT.

ACCESSION VERSION KEYWORDS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www-seg.wi.mit.edu
Birren, B., Nusbaum, C. and Lander, E. Mus musculus, clone RP23-223N19
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                                                                                                                                                                                                                                                                          7.6%; Score 101.8; DB 2; Length 267182;
43.0%; Pred. No: 1.2e-11;
tive 0; Mismatches 567; Indels 21;
                                                                                                                 91514. 117047

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165929. 221922

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              arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
    known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91413: contig of 10117 bp in length 91513: gap of 100 bp 117047: contig of 25534 bp in length 117147: gap of 100 bp 165828: contig of 48681 bp in length 165928: gap of 100 bp 221922: contig of 55994 bp in length 222022: gap of 100 bp 27182: contig of 45160 bp in length 27182: contig of 45160 bp in length.
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48: contig of 8097 bp in ...
248: gap of 100 bp
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contig of 14948 bp in length
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of 10274 bp in length
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y of 8375 bp in length
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gap of 100 bp
contig of 1064 bp in length
contig of 1889 bp in length
gap of 100 bp
contig of 1389 bp in length
contig of 1328 bp in length
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of 4288 bp in length
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45.4%; Pred. No. 2e-11;
tive 0; Mismatches 662;
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fragment chain:<u>1</u>
clone_en<u>0</u>:17
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fragment chain:3
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Best Local Similarity 45.45
Matches 566; Conservative
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                                               1051 CAGGGGGGAAAAAGGGACCGAAAAACCCAGCCCACCCGAGAAGGA------GACAGC 1102
                                                                                                                                                                                                    AL691432 189129 bp DNA linear HTG 03-JUL-2004
Homo sapiens chromosome l clone RP11-345P4, WORKING DRAFT SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 189129)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (02-JUL-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Jul 5, 2004 this sequence version replaced gi:49658403.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 50% of reads
Chemistry: Dye-terminator Big Dye; 49% of reads
Consensus quality: 185111 bases at least Q40
Consensus quality: 185111 bases at least Q30
Consensus quality: 186474 bases at least Q30
Insert size: 188129; sum-of-contigs
Insert size: 148416; 30.5% error; agarose-fp
Quality coverage: 13.14x in Q20 bases; sum-of-contigs Quality
Coverage: 18.29x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
Homo sapiens (human)
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AC103465_1 200001 310000
AC103465_3 300001 410000
AC103465_4 400001 452732
Continuation (4 of 5) of AC103465 from base 300001 (AC103465 Rattus norvegicus clone CHZ
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Pred. No. 2.7e-11;
0; Mismatches 553;
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Best Local Similarity 45.7%;
Matches 482; Conservative
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Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., Macdean, C., Macdonald, P., Major, J., Marquis, N., Mathews, C., Mihova, T., Macdean, P., McRennan, K., Meldrim, J., Mathews, C., Mihova, T., Menga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Meall, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Seman, S., Sevetti, M., Ropy, A., Schusge-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Viel, R., Yo, A., Wilson, B., Wu, X., Myman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. V., Young, G., Submission.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unrect Submission

Submitted (20-APR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

12 (Dases 1 to 132080)

Sa Irren,B. Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V. Bloom,T., Boguslavkiy,L., Chang,J., Chazero,B., Chopel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dear,J.S., Dodge,S., Gord,S., Gordete,M., Graham,L., Grand,Pierre,N., Diaz,J.S., Dodge,S., Gord,S., Gordete,M., Graham,L., Grand,Pierre,N., Galagan,J., Gandyna,S., Ginde,S., Gordete,M., Hulme,W., Iliev,I., Johnson,R., Johnson,R., Jones,C., Landers,T., Lehoczky,J., Levine,R., Lindblad-Toh,K., Liu,G., Macdonald,P., Malle,R., Lindblad-Toh,K., Liu,G., Macdonald,P., McKernan,K., Maldrim,J., Mathews,C., Mibova,T., Mangaly, W., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Connell,P., O'Neal,D., Colliver,J., Peterson,K., Phurkhang,P., Pierre,N., Pollara,V., Raman,J., Peterson,K., Phurkhang,P., Pierre,N., Schauez,R., Vola,R., Willow,R., Wallow,R., Yell,R., Vola,R., Wilson,B., W., Wallow, N., Yell,R., Wallow,R., Zahonu,J., Yellow,R., Sulancy,R., Shauez,R., Sulancy,R., Vola,R., Wilson,B., W., Wanan,D., Yel,W.J., Young,G., Direct Submission

Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: sequence submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center code: WIBR
Web site: http://www-seq.wi.mit.edu
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/clone lib="CITD1 Human BAC"
438 . 602
/rpt_family="MER5B"
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/rpt_family="L3"
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Center clone name: 2017_F_17
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/db_xref="taxon:9606"
/chromosome="15"
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1044 AACAACCCAGGGGGCAAAAGGGACCGAAAAACCCAGGCCCAGGCCGAGAAGGAGAGAGCC 1103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACU609368 132080 bp DNA linear PRI 15-MAY-2002
Homo sapiens chromosome 15, clone CTD-2017F17, complete sequence.
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Changaler, B., Charar, B., Camarata, J., Camarata, J., Camarata, J., Camarata, J., Cook, A., Cook, P., Chararo, B., Chararo, B., Charalano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                1104 AAGCACAAAAAGGGCAACA----AAGGGGAAGGGCCAAAAAGCACCCCAACGAAAAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 132080)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 15, clone CTD-2017F17
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us-10-019-341-4\_copy\_256\_1599.rge

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                                                                   Gaps
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                                                     7.4%; Score 99.6; DB 9; Length 1
46.5%; Pred. No. 3.6e-11;
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Best Local Similarity 46.5
Matches 427; Conservative
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9: gap of unknown length
9: contig of 1201 bp in length
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12: gap of unknown length
13: gap of unknown length
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Consensus quality: 175579 bases at least Q30
Consensus quality: 186949 bases at least Q30
Consensus quality: 186949 bases at least Q30
Estimated insert size: 293091; sum-of-contigs estimation
Quality coverage: 293091; sum-of-contigs estimation
Quality coverage: 3.28 in Q20 bases; sum-of-contigs estimation
* NOTE: This is a 'working draft' sequence. It currently
* consists of 101 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (17-NOV-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. DOB Joint Genome Institute.
                                                                                            AC084799
303091 bp DNA linear HTG 17.
Mus musculus chromosome 16 clone RP23-197M9, WORKING DRAFT
SEQUENCE, 101 unordered pieces.
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contig of 1320 bp in length
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secontig of 1074 bp in length
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DOB Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Project Information
Center Project Name: 0
Center clone name: RPCI-23_197M9
                                                                                                                                                    AC084799.1 GI:11192127
HTG; HTGS_PHASE1; HTGS_DRAFT.
Mus musculus (house mouse)
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                                                       RESULT 11
AC084799
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AUTHORS
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REFERENCE
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                                                                                                                                                       VERSION
KEYWORDS
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AC073957 196204 bp DNA linear PRI 09-JAN-2002
Homo sapiens BAC clone RP11-449P15 from 7, complete sequence.
AC073957
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Submitted (07-JUJ-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (29-NOV-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                          94460
                   94042 CACAAGAAGAAGGCGACAGCAAAGAAAGAGCGA-AGGAAGACCAGAAGGAGGGAAAAAA 94100
                                                                             1089
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Catarrhin; Hominidae; Homo.
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2 (bases 1 to 196204)
Leonard, S., Cotton, M., Hawkins, M. and Spalding, L.
The sequence of Homo sapiens BAC clone RP11-449P15
Thoublished (2001)
3 (bases 1 to 196204)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
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Mammalia, Burheria, Primates,
1 (bases 1 to 196204)
Sulston, J.E. and Waterston, R.
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Waterston, R.H.
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/note="similar to Mus musculus EST AA021831 (NID:g1485585)
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7108. 7135
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/hote="match to EST BF814714 (NID:g12147717)"
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/note="match to EST BF874571 (NID:g12264701)"
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5193. .5455
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/hote="match to EST AW877271 (NID:g8015626)"
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/rpt_family="(CACCC)n"
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                                                                                                                                                                                                          Direct Submission
Submitted (09-JAN-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Nov 29, 2001 this sequence version replaced gi:14589737.

Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
                                                                   Direct Submission
Submitted (03-JAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
6 (bases 1 to 196204)
Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHCRI Chromosome 7 Mapping Project (Exic D. Green, Director), John D. McPherson in the Droject (Exic D. Green, Director), John D. McPherson in the University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7, send mailto:egreen@nhgri.nih.gov, or see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, B., Tateno, M., Catanese, J.G. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 5:1-8. The clone may be obtained either from and coworkers at the Roswell Park Cancer Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The clone sequenced to the left is RP11-1244M4; the clone sequenced to the right is RP13-580H13. Actual start of this clone is at base position 1 of RP11-449P15; actual end is at base position 196204 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Data from AC091729 was used to finish this clone, AC073957.
Polymorphisms have been identified between AC073957 and AC091729.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center project name: H_NH0449P15
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mol_type="genomic DNA"
db_xref="taxon:9606"
/chromosome="7"
                                                                                                                                                                                                                                                                                                                                                                                                                                            Summary Statistics
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VECTOR: pBACe3.6
NEIGHBORING SEQUENCE INFORMATION:
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MO 63108, USA
5 (bases 1 to 196204)
Waterston, R.H.
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FEATURES

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ACU/9417 130540 bp DNA linear HTG 01-SEP-2000
Mus musculus chromosome 16 clone RP23-102A24, WORKING DRAFT
SEQUENCE, 34 unordered pieces.
                                                                                                                                                                                                                                                                                              Mus musculus
Mus musculus
Mus de Alexandra, Craniata; Vertebrata; Euteleostomi;
Musmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
1 (bases 1 to 130540)
10 (bases 1 to 130540)
Sequencing Genome Institute.
Sequencing of Mouse
                                                                                                                                                                                                                                                1049 CCCAGGGGGGAAAAAGGGACCGAAAAAACCCAGCCACCCGAGAAGGAGAAGGACAAGCA
                                                                                                             27274 GAGAAAGGGAAAAGGAGAAAAG-GAGAAAGGGAGAAAGGAGAAAGGAGAAAGG
                                                                                                                                                                                                                             1109 CAAAAAGGGCAACAAAGGGGGGAAAAA--GCACACCCCAACGAAAAAGACAGGGACA
                                                                 GAACACCAGGAAGCCAAAGGAAGAGACAACAG-CGGCAGACGGGGAGCAGCCCGGCCGC
                                                                                                                                    AA-GACACGGGAACGAGGAAACCCAACCAACAGGCCGAGACCGAGGCACCGGGCCGAGA
                                             Summary Statistics
Consensus quality: 71349 bases at least Q40
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Center Project Name: 0
Center clone name: RPCI-23_102A24
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HTG; HTGS PHASE1; HTGS DRAFT.
Mus musculus (house mouse)
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TITLE
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AC079417
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                                                                                                                                                                                                                                                                          /note="similar to Mus musculus EST AA087576 (NID:g1630844)
                                                                                                                                                                                                                                                                                                                                                                                                                                  CGCACGGGCCAGGAGCAACCCAGGCCGCGGGCACCCAAACGGG---GGACAGGAGGGCC 214
                                                                                                              note="similar to Mus musculus EST AA021831 (NID:g1485585)
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Pred. No. 8.7e-11;
0; Mismatches 627; Indels 16;
                                                                                                                                                                                                                 note="match to EST BI084297 (NID:g14502627)"
                                                                                                                                                                                           note="match to EST BG768797 (NID:g14079450)"
                                                                  'note="match to EST BG709448 (NID:g13987794)"
                                                                                                                                              note="match to EST BF087410 (NID:g10893120)"
646. .7711
                                                                                                                                                                      (NID:910368069) "
                       (NID:g11601773)"
                /630. .7711
/note="match to EST BF516594 (NID:g11601773)"
6300. .7711
/note="match to EST BG034421 (NID:g12427714)"
                                                                                                                                                                                                                                         note="similar to Gallus gallus EST AJ396197
                                                                                           note="match to EST T16043 (NID:9518205)"
                                                                                                                                                                        note="match to EST BE855648
                                                                                                                                                                                                                                                        "(NID:97127890)"
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Best Local Similarity 47.4%;
Matches 580; Conservative (
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Consensus quality: 83788 bases at least Q30
Consensus quality: 89369 bases at least Q20
Estimated insert size: 93300; agarose-fp estimation
Estimated insert size: 93300; agarose-fp estimation
Quality coverage: 3.69 in Q20 bases; sum-of-contigs estimation
Quality coverage: 2.7 in Q20 bases; sum-of-contigs estimation
* NOTE: This is a "working draft" sequence. It currently
* consists of 34 contigs. The true order of the pieces
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
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/clone="RP23-102A24"
/clone_lib="RPCI mouse BAC library 23"
                                                                                                                                                                                                                     Score 97.6; DB 2; ]
Pred. No. 9.7e-11;
]; Mismatches 587;
                                                                                                       1. .130540
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
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Submission
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Submitted (03-FEB-1999) Drosophila Genome Center, Lawrence Berkeley
Laboratory, MS 64-121, Berkeley, CA 94720, USA
CO 13m 31, 2000 this sequence version replaced gi:6587780.
Or gan 31, 2000 this sequence version replaced yi:6587780.
Or further information about this sequence, including its location
and relationship to other sequences, please visit our sequence
archive Web site (http://www.fruitfly.org/sequence/) or send email
to bdgp@fruitfly.berkeley.edu. All contigs in this submission meet
the following cutoffs: length >= 200 bases.
* NOTE: This is a working draft' sequence. It currently
* consists of 38 contigs. The true order of the pieces
* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster chromosome 3 clone BACR48113 (DS22) RPCI-98 48.11.13 map 90E1-90F10 strain y; cn bw sp, *** SEQUENCING IN AC006495
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cenliker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G. Butenhoff, C., Champe, M., Chavez, C., Chew, M., Clesiolka, L., Boyle, C.M., Farfan, D.E., Galle, R., Gacorge, R.A., Harris, N.L., Hinkle, A., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kaarney, L., Lee, B., Lewis, S., Li, P., Ling, H., Moshrefi, A.R., Nixon, K., Pacleb, J.M., Paxk, S., Pfeiffer, B., Mochrefi, M., Nixon, K., Pacleb, J.M., Paxk, S., Pfeiffer, B., Woolley, P., Yang, S., Yee, M., Yu, C. and Rubin, G.M. Better, D., Sequencing of Drosophila melanogaster
                                                                                                                                                                   959 AGACAAGCCGAAAAGAAGCAGGCGAAACGGGCGAACAAGAACAAAGAACGGCAGGAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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s: contig of 6337 bp in length
s: gap of unknown length
s: contig of 5481 bp in length
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of 440 bp in length
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/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/mol_type="genomic DNA"
/strain="Y; cn bw sp"
/db xref="taxon:7227"
/chromscome="3"
/map="90El-99010"
/clone="BACR48113 (D522) RPCI-98 48.1.13"
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                                                                                                                                                                                                                                                                                                               7.2%; Score 97.4; DB 2; Length 155840; Conservative 0; Mismatches 409; Indels 11;
 154319: contig of 649 bp in length 154399: gap of unknown length 154743: contig of 344 bp in length 154823: gap of unknown length 155522: contig of 599 bp in length 155502: gap of unknown length 155804: contig of 338 bp in length 155804: contig of 338 bp in length
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                                                                                                         Location/Qualifiers
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ROD 15-MAY-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The RPCI-24 BAC Library has been constructed by Pieter de Jong and coworkers (http://www.chori.org) from male C57BL/6J mouse spleen and/or brain genomic DNA. The clone and detailed information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome Sequencing Center, 4444 Forest Park
3108, USA
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Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                 AC147269
Mus musculus BAC clone RP24-281E6 from chromosome 18, complete
                                            Center: Washington University Genome Sequencing Center Center code: WUGSC Web site: http://genome.wustl.edu Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (15-MAY-2004) Genome Sequencing Center, 4444 For
Parkway, St. Louis, MO 63108, USA
On Mar 6, 2004 this sequence version replaced gi:39979572.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Berghoff, A., Haglund, K. and Bielicki, L.
The sequence of Mus musculus BAC clone RP24-281E6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (06-MAR-2004) Genome Sequencing Center,
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Mus musculus
Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
1 (bases 1 to 177277)
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4 (bases 1 to 17727)
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obtained from Pieter de Jong and coworkers at http://www.chori.org
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
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/db_xref="taxon:10090"
/dbone="RP24-2B186"
/clone="RR24-2B186"
/clone="RR21-24"
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/product="tRR01-24"
/product="tRNA-Ser"
/note="tikely pseudogene (HMM Sc=32.06 / Sec struct Sc=10.06)"
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                NEIGHBORING SEQUENCE INFORMATION:
This sequence is the entire insert of the clone. This clone overlapped by AC139334.

1. 177277
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                                                                                                                                                                  7.2%; Score 97.2; DB 10; Length 46.8%; Pred. No. 1.2e-10; Live 0; Mismatches 423; Indels
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- nucleic search, using sw model OM nucleic

Run on:

October 20, 2004, 17:04:23 ; Search time 728 Seconds (without alignments) 9691.239 Million cell updates/sec

US-10-019-341-4\_COPY\_256\_1599 1344 Perfect score:

l aagacacagcgaggacacgc.......gagaagaagaagaaccccgc 1344 Sequence:

IDENTITY NUC Gapoxt 1.0 Scoring table:

4134886 segs, 2624710521 residues Searched:

Total number of hits satisfying chosen parameters: Minimum DB Maximum DB

8269772

seq length: 0 seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqn1990s:\* geneseqn2000s:\* geneseqn2001as:\* geneseqn2001bs:\* geneseqn2003cs:\* geneseqn2003ds:\* geneseqn2002as:\* geneseqn2002bs:\* geneseqn2003as:\* N\_Geneseq\_23Sep04:\* geneseqn2003bs:\* geneseqn2004s:\* genesegn1980s:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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## ALIGNMENTS

Lipoprotein lipase; LPL; S447X; cardiovascular; diabetes; obesity; AAF28296 standard; RNA; 2565 BP. entry) (first deficiency; ss. 05-APR-2001 AAF28296; LPL mRNA. 

WO200100220-A2. Homo sapiens

04-JAN-2001

23-JUN-2000; 2000WO-CA000762. 99EP-00202048. 24-JUN-1999;

(UYBR-) UNIV BRITISH COLUMBIA. (AMST-) AMSTERDAM MOLECULAR THERAPEUTICS ! (UYAM-) UNIV AMSTERDAM ACADEMIC HOSPITAL.

BV.

Kastelein JJP; Hayden MR,

WPI; 2001-112388/12.

Use of lipoprotein lipase S447X therapeutic for the preparation of a pharmaceutical composition for the treatment of coronary heart disease, atherosclerosis, angina pectoris, hypertension, diabetes, cachexia and

Claim 5; Fig 4; 51pp; English.

The present invention relates to use of a lipoprotein lipase (LPL) S447X therapeutic for the preparation of a pharmaceutical for the treatment of an LPL-responsive condition. Diseases that may be treated are complete LPL deficiency, chylomicronemia, hyperlipidemia, partial LPL deficiency pancreatitis, hypertriglyceridemia, hypoalpha-lipoproteinemia (low high density lipoprotein-cholesterol), cardiovascular disease, coronary heart

1260 1515

1200 1455

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This sequence represents a gene encoding a subunit of the cellulose synthase complex of Vigna angularis. The invention relates to subunits cellulose synthetic equipment, that can be used to increase the amount can lose synthesised by a plant. The proteins and genes encoding them can also be used to improve the properties of the cellulose being produced by a plant.
                                                               GAAAAAAGGCCCCAGGGCGAGGCCAAGCCAAAGGAGAACCCCAAAGGAACGGACCGGAC
                                                                                                                    GAGGCCCCAAACACCCAAGCCCCAAGAAACAGAAAAAGCCCCGCGGGCACGAACAGACCACACACA
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disease, coronary artery disease, atherosclerosis, angina pectoris, hypertension, cerebrovascular disease, coronary restenosis, peripheral vascular disease, diabetes, cachexia or obesity
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                                        Length 2565;
                           0 Other;
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                                        100.0%; Score 1344; DB 4;
100.0%; Pred. No. 9.4e-278;
ive 0; Mismatches 0;
                           2565 BP; 1020 A; 739 C; 806 G; 0 T; 0 U;
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Matches 1344; Conservative
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GNHASTRASGTHRARGSRASGYGGASNGTHRHSVAGYSGARGHSRARGGASNSRSRRGNV 10194
                                                                                                                                                                                                                                              BacRI; bacteriocin; antimicrobial; antibacterial; antibiotic;
Moraxella bovis; infectious bovine keratoconjunctivitis; cancer; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This polynucleotide comprises the bacteriocin BacRI operon of Staphylococcus aureus UT007. The sequence of the BacRI operon was determined by N-terminal sequencing of purified BacRI peptide (see AAW54171), with back-translation and plasmid analysis. The BacRI operon includes the BacRI gene (see AAV21510), a homologue of the cylm gene of the cytolysin operon of Enterococcus faecalis whose function is involved bit the maturation of pre-cytolysin, an ATP-transporter gene, biol and biol genes related to lactococcin biosynthesis and modification, and gene involved in immunity function. BacRI peptides can be produced by construction of an expression vector containing an oligomucleotide or operon coding for BacRI, and use of the vector to transform host cells for BacRI expression. The entire BacRI operon has been cloned into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Therapeutic proteinaceous substances from Staphylococcus aureus - useful to inhibit growth of wide range of prokaryotic or eukaryotic cells, e.g. Moraxella bovis causing infectious bovine keratoconjunctivitis.
                              AGCGCAGAGAAAAAAGGCCCCCAGGGCCGAGGCCAAGCCAAAGGAGAACC
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The present invention relates to methods for amplifying nucleic cells, for isolating artificial chromosomes, and preparing cell
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   recombinant BacRI peptide into the medium. Bacteriocin BacRI is active against many Gram-positive and Gram-negative organisms such as Bordetella bronchoseptica, Pasteurella multocida and Staphylococcus aureus; Moraxella bovis, causing infectious bovine keratoconjunctivitis, is especially sensitive. BacRI can also be used as an anti-cancer agent. (Updated on 17-OCT-2003 to standardise OS field)
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                                                                                                                                                                                                                                                     AAAAGGAGCGCAGAGAAAAAAGGCCCCAGGGCGAGGGCCAAGCCAAAGGAGAACCCCAAA
                                                                                                                                                                                                                                                                                   Amplifying nucleic acid for constructing artificial chromosomes, comprises introducing a DNA fragment into a cell to incorporate the into a chromosome, and identifying cells with chromosomes that has
                                                                                                                                                                                                                                                                                                                   GGAACGGACCGGACGCCCCAAACACCAAAGCCCCAAGAAACAGAAAAGCCCGG
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96US-00682080.
96US-00695191.
97US-00835682.
2000US-00724693.
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ID ABX11086 standard; DNA; 42999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human ribosomal RNA (rRNA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entry)
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07-AUG-1996;
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                                                                                 The first intervent of the invention also discloses cells and cell lines that contain the nucleic acids or artificial composemes. The methods of the invention are useful for amplifying chromosomes. The methods of the invention are useful for amplifying nucleic acids in cells, in generating and isolating artificial chromosomes (e.g. mammalian artificial chromosomes or MACS), and in cells with the chromosomes to selected cells and tissues. The artificial chromosomes are useful in gene therapy, gene product production systems, production of humanised genetically transformed animal organs, production of transgenic plants and animals that would employ chromosomal elements of transgenic plants and animals that would employ chromosomal elements as information storage wehicles, for analysis and study of centromere function, for the production of artificial chromosomes. The present companion of the present invention. Note: All N uncleotides (EXCEPT those at positions 21526-21527, 23183, 24977-24977, 28699, 28945, 34074 and 34474) have been added to the sequence by the indexer to match the number of bases this sequence is listing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25912 AAAĠACAĠAĠAĊĀĠACAGĀGAGAĀACAGĠĊĀĠAĀĠĀGĀGĀĠĀĠĀĠĀĠĀĠNNNNĀGĀĊ 25853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25852 AĞTAAAĞGAGAĞAĞAĞAĞAĞAĞAĞAĞAĞĞĞAĞAAĞAATAAĞAĞĞAĞANNNIĞAÇA 25793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25673 ACAGGCAGAGAGAGAGAGAGTAGCGAGAGAAACAGAAAAGGTAGGGAGAGANNNNGAG 25614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                that contain artificial chromosomes. The methods comprise introducing a DNA fragment comprising a selectable marker into a cell, growing the cell under selective conditions to produce cells that have incorporated the DNA fragment or its portion into a chromosome, and identifying from among the resulting cells those that include a chromosome or its fragment with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25553 GAGAGACAAGGAGAGAGAGAGAGAGAGAGACAGAGACAGAGAGAGAGACAGACNNNGAA 25494
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                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 42999 BP; 5970 A; 12784 C; 10787 G; 10765 T; 0 U; 2693 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        336 GAGCAGAAGCCCCCGAGGCGCCCCGAGAGAGACGCACACACACACACAGAGGGCCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25733 AAAGAGACAGACAGACAGAGAAAGAGACAGACAGAGAAAAGACAGAGAGAGAAANNNGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGCCCACACCCACGACCCGGAAGAAAACCAAGAAGGCCACAGGGCAGCCAAGGAAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.2%; Score 97; DB 8; Length 42999;
42.2%; Pred. No. 6.8e-11;
iive 0; Mismatches 669; Indels 2:
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Best Local Similarity 42.2.
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25029 AGTGAGAAANNNCAGAAAGAGAGGGAGACAGAGAAAAAGAGACAGGGGANNAGAGA 24970
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                                                                                                       24856 GAGACACAGAAAAGANNNNGAGGGCAGACAGACAGAAAAGAAAAGAAAAA 24799
                                                                                                                                                                                                                                                                                                                                                                                                                                 1236 AGAACCCCAAAGGAACGGACGGACGAGGCCCCAAACACCCAAGGCCCCAAGAAACAGAAA 1293
                         1056 GGGGCAAAAGGGACCGAAAAACCCAGCCCACCGAGAAGGAGACAGCCAAGCACAAAAAG
                                                                                                                                                                                                                                                                                                                        GGCAACAAAGGGGAAAAAAGCACACACCCCAACGAAAAGACAGGAACAGAAAAAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antisense oligonucleotide; multiple target; antisense treatment; impaired respiration; inflammation; lung disease; pulmonary vasconstriction; inflammation; allergic rhinitis; acute asthma; allergy; asthma; impeded respiration; respiratory distress syndrome; pain; cystic fibrosis; pulmonary bypertension; pulmonary vasconstriction; emphysema; chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma; colon cancer; breast cancer; lung cancer; pancreatic cancer; hepatic cancer; hepatic cancer; melanoma; hepatic metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human adenosine Al receptor antisense oligonucleotide fragment.
                                                                            GAGAAAGGGACAGACAGAGAGACAGAGAGAGAGAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAX53491 standard; DNA; 114955 BP
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ID AAX53
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10-APR-1996; 96US-00629822.
15-UUL-1996; 96US-00682080.
07-AUG-1996; 96US-00695191.
10-APR-1997; 97US-00835682.
28-NOV-2000; 2000US-00724693.
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                                                                                   The specification describes antisense oligomucleotides (AAX52869-X55271)

directed against at least 2 mRNAs selected from target genes, coding and
con-coding regions of RNAs corresponding to target genes, coding and
codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'
codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'
codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'
codons, mixtures. The entisense oligomucleotides may be derived
from sequences AAX55272-74. These multiple target oligomucleotides
conditions or mixtures. These multiple target oligomucleotides
from sequences AAX55180-271) can be used for the antisense treatment of
diseases and conditions. Typical diseases and conditions are those
associated with impaired respiration and inflammation, including lung
diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,
acute asthma, allergies, asthma, impeded respiration, respiratory
diseases (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.
colon cancer, breast cancer, lung cancer, panceratic cancer,
colon cancer, breast cancer, lung cancer, melanoma, hepatic metastases,
electronic and an all types of cancers which may metastasize or have metastasized
colon cancer such as all types of cancers which may metastasize or have metastasized
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                       antisense oligonucleotides used in treatment of, e.g. pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                       25;
                                                                                                                                                                                                                                                                                                                                                                                                                            Length 114955;
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 7.2%; Score 97; DB 2; Length 1145
Best Local Similarity 36.1%; Pred. No. 8.3e-11;
Matches 449; Conservative 213; Mismatches 558; Indels
                                                                   Disclosure; Page 37; 120pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GACCACANHININSCGCCCGGAGACCCINIHININSCGCCCGGAGACCCINIHININSCCVCGV
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GACGGGGAGCAGCCCGGCCACAG---AAGACAGAAAAGCAGGAGAGACAAAA
                                                                                                                                                                                                                                                                                                                                                                                   AGGGACCGCAGGGAGAAAGGCCAGCAGAAAGGAAAGGCACCGCG-GAGGAAAGCCAGACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1022 GAAGAAGGGAGGAAGAACAACCCAAGGGGGGGGCAAAAGGGACCGAAAAACCCAG
                                                                          ACAGCACAAAVCVAAGCAAVCAVGGAVGNNHNNNSTCCTCAAA 86343
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24865 ACAGACAGAGAGACACAGAAAAAAAAAAGAAAGGGCAGACAGACAGAGAGAGAGACAGAT 24806
                                                                                                                                                                                                                                                                                                                                                                                                            satellite artificial chromosome; minichromosome; euchromatin;
neo-chromosome; neocentromere; gene therapy;
pericentromeric heterochromatin; ribosomal DNA complete repeating unit.
                                                                                                                                                                              GCCACAGAAGACAGAAAAAGGAGGAGACCAGAAAAAGGGACCGCAGGGAGAAAAGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human; mammalian artificial chromosome; SATAC;
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96US-00695191.
97US-00835682.
2000US-00724693.
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10-APR-1997;
28-NOV-2000;
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15-JUL-1996;
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                                                                                                                                                       The invention relates to a method of amplifying a nucleic acid. The method comprises introducing a nucleic acid into a plant cell where the introduced molecule includes a sequence targeting it to an amplifiable region of the cell chromosome then growing the cell and identifying cells that include a chromosome including a portion that has undergone amplification. The targeting sequence is selected from those that target the nucleic acid to the pericentric heterochromatic region of a chromosome and preferably comprises rDNA, an origin of replication, or an nucleic acid (preparing artificial chromosomes) in plant cells. The
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                                                                          Amplifying nucleic acid comprises introducing a nucleic acid molecule into a plant cell, growing the cell and identifying from among the resulting cells those that include a chromosome with a portion that has
                                                                                                                                                                                                                                                                                                                                                                GGGCCCGGACAACGGAGGAGGAGAACACCCCGGGACAAGCCACCGGGAACAGCCGGAG
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                                                                                                                                                                                                                                                                                                                                                 32;
                                                                                                                                                                                                                                                                                                                    7.1%; Score 94.8; DB 9; Length 41907; llarity 45.3%; Pred. No. 2e-10; Conservative 0; Mismatches 655; Indels 32;
                                                                                                                                                                                                                                                                       present sequence represents the human rDNA repeat unit.
                                                                                                                                  Disclosure; Page 76-94; 108pp; English.
                                                                                                               undergone amplification.
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The invention relates to preparing cells or cell lines comprising cintroducing a mammalian artificial chromosome that a comprises a nucleic acid encoding a therapeutic product or a gene product into a cell or tissue of a host animal. The artificial chromosome is a mammalian SATAC (satellite artificial chromosome) or a minichromosomes based on cubromatin (e.g. a neo-chromosome and which comprises a neocentromere). The method is useful for preparing cells or cell lines which may be employed in cell-based methods for production of heterologous proteins, gene therapy, or generation of transgenic non-human animals. The cells or cell lines are also useful for cell fusion, as recipient cells for donor DNA encoding a gene or multiple genes, or for delivery of heterologous DNA into cells. The present sequence is the Human ribosomal DNA complete repeating unit, useful for targeting artificial chromosomes to
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                                                                                          Preparing cells or cell lines for use in cell-based methods for heterologous protein production or gene therapy, by introducing a minichromosome or a mammalian satellite artificial chromosome into a cell
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Pred. No. 2e-10;
0; Mismatches 655;
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                                                                                                                                                                      Disclosure; Page 76-95; 109pp; English
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HADLACZKY G.
SZALAY A A.
                                                                                                                                           tissue of a host.
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                                                                                          Attention deficit hyperactivity disorder; ADHD; hypertension; invertebrate foraging behaviour; nitric oxide; hypotensive; cGMP-dependent protein kinase; human; neuroleptic; ds; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                          Invertebrate foraging behaviour associated human DNA sequence #12
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                                                GCCACAGAAGACAGAAAAGCAGGAGAGCCAGAAAAAAGGGACCGCAGGGAGAAAAGGCC
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96US-00682080.
96US-00695191.
97US-00835682.
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15-JUL-1996;
07-AUG-1996;
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28-NOV-2000;
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                                                                                                                                                                    The present invention relates to a method of identifying a compound that modulates attention deficit hyperactivity disorder (ADHD) in a mammal. The method comprises administering a test compound to an invertebrate, and measuring a foraging behaviour of the invertebrate, where the compound that modulates the foraging behaviour of the invertebrate is characterised as a compound that modulates ADHD in a mammal. The compound treating ADHD, hypertension or other diseases associated with a nitric oxide/CGMP-dependent protein kinase network in a mammal, particularly humans. The method distinguishes a compound that has a specific effect on dependent kinase protein network in a mammal from a nitric oxide/CGMP-abendent brosen in a mammal from a compound that has a specific effect on dependent kinase protein network in a mammal from a compound that has a sassociated with a nitric oxide/CGMP-abendent brosen bressel by present sequence represents a DNA sequence a passociated with a nitric oxide/CGMP-abendent hinser presents a publication or other diseases associated with a nitric oxide/CGMP-abendent hinser present sequence represents a DNA sequence and associated with a nitric oxide/CGMP-abendent hinser presents sequence represents a DNA sequence and associated with a nitric oxide/CGMP-abendent hinser and associated with a nitric oxide/CGMP-abendent hinser as a compound that has a present sequence and associated with a nitric oxide/CGMP-abendent hinser and a nitric oxide/CGM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCCAG----CGCGGCAGCAGGAAGCGACCAAAAGAAAGCAACAGAAACGGCCCGACCAGCG 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    446
                                                                  Identifying a compound that modulates an attention deficit hyperactivity disorder (ADHD) for treating e.g. ADHD or hypertension, comprises measuring a foraging behavior an invertebrate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    627 AAGCAGAGCCAAAAGAAGCAGCAAAAGACCGAAGACCGCCAGAGCCCAAAGCCCAACC 686
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 6; Length 42999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 94.8; DB 6; Length 4;
Pred. No. 2e-10;
0; Mismatches 655; Indels
                                                                                                                                                                                                                                                                                                                                                                                                 associated with invertebrate foraging behaviour
                                                                                                                                     Claim 89; Page 182-195; 246pp; English
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Best Local Similarity 45.3%;
Matches 568; Conservative 0
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24865 ACAGACAGAGAGACACAGAAAAAAAAGAGAGAGGGCAGACAGAGAGAAAAGAGACAGAT 24806
                                                                                                                          This sequence represents a gene encoding a subunit of the cellulose synthase complex of Vigna angularis. The invention relates to subunits cellulose synthesize equipment, that can be used to increase the amount callulose synthesized by a plant. The proteins and genes encoding them can also be used to improve the properties of the cellulose being produced by a plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for the improvement
                                                                                                                                                                                                                                                                                                                                                                            1047 AACCCAGGGGGGAAAAAGGGACCGAAAAAACCCAGCCCACCCGAGAAGGAGACAGCCAAG
                                                                                                                                                                                                                                                      GAMAAGGCGGCCGAGAAAAAAAGGAGCGCAGAGAAAAAAAGGCCC---CAGGGCGAAGG
                                                                                                                                                                                                                                                                               <u> AGACAGACAGACAGACAGGAGAGGAGGAGTAAGACAAAAGATACACAGAGA</u>
                                                                                                   1107 CACAAAAAGGGCAACAAAGGGGAAGGGCCAAAAGCACCCCCAACGAAAAAGACAGGACA
                                                                                                                                                                                                                              867 GCCACAGAAGACAGAGAAAAGCAGGAGAGCCAGAAAAAGGGACCGCAGGAGAAAAAGGCC
                                                                                                                                                                                                                                                                                                                                                            CAAGAAACAGAAAAGCCCGCGGCACGAACAGACCACACACACAGAGAGAGAGA
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the amount of cellulose synthesized in a plant body.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene encoding a subunit of cellulose synthase.
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OJI PAPER CO.
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P-PSDB; AAY85180.
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                                                                                                                       The present invention relates to novel pure plant satellite artificial chromosome (SATAC). Sequences of the invention are useful for producing transgenic plants and gene products. They are also useful for cloning a centromere from a plant. The present sequence is human ribosomal DNA (rDNA) repeat region used in the exemplification of the invention
                                               chromosome useful
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                                      for producing transgenic plant satellite artificial chromosor for producing transgenic plant, producing gene product, cloning centromere from plant.
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al Similarity 45.3%;
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                                                   295 AAAAGAAAGCAACAGAAACGGCCCGACCAGGGGACCAACGAGAGCAGAGCCCCGAGGGC 354
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                                                                                                                         5748 VAASNHTHRRASNASNYSRARGMTTYRSRHSARGASRSRARGYSGSRGYAAGYA-SNHYSA
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      Sequence 6741 BP; 1712 A; 870 C; 1468 G; 1374 T; 0 U; 1317 Other;
                         Length 6741;
                                       Indels
                                       485;
                       91.2; DB 3;
No. 8.1e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 91.2; DB
Pred. No. 8.1e-1
                            Similarity 18.7%; Pre 95; Conservative 355;
                       6.8%;
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/note= "this nucleotide is represented as a * in the
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298 AGAAAGCAACAGAAAGGGCCCGACCAGCGGACCAACGAGAGCAGAAGCCCCGGAGCGCCCC 357
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larity 21.4%; Pred. No. 2.2e-09;
Conservative 278; Mismatches 401; Indels
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9; Gaps

overexpressed in ovarian

isolated nucleic acid molecules (markers)

2000US-0191031P. 2000US-0207124P. 2000US-0211940P. 2000US-0216820P. 2000US-0220661P.

2000US-0257672P

Lillie J;

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cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.
                                                                                                                            Disclosure; SEQ ID NO 21388; 106pp; English.
                                                               (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
         21-MAR-2001; 2001WO-US009126
                                                                                        WPI; 2001-611502/70,
                          25-MAY-2000;
15-JUN-2000;
07-JUL-2000;
25-JUL-2000;
                                                    21-DEC-2000;
                                                                            Lee J,
                                                                                                    Novel
  | ::| |:: :: |:|: : |:| : | GSYBDATASSGBANYHSSYBTCKARGARCKDSNCYATKYHNTNTKDSSYBTCKARGDAWS 4153
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                                                                 GAAGAAAACCAAAGAAGGCCACAGGGAGCCAAGGAAGCCGAGAAAGGCCGCGCGCGAGAAA
                        AAGACCGCCAGAGCCCACAAAGCCCAAAGAAAGACACGGGACGAGAGAAACCCAAAC
                                                                                                                                         718 CAACAGGCCGAGACCGAGGCACGGGCCGAGAGGAGAACACCCACACCGCGGAAGCCACA
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AVAVAVNAVAVNAVAVNRCKDDAWSNGSYBDATAS 3587
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The invention relates to nucleic acid markers which are overexpressed in cancer cells as compared to their expression in normal (i.e. non-cancerous) ovarian cancer cells. The invention also relates to polypeptides cancerous) ovarian calls. The invention also relates to polypeptides cancerous by the markers, antibodies that selectively bind to the cancerous ovarian cancer involving inhibiting expression of a gene of developing ovarian cancer involving inhibiting expression of a gene of patient afflicted with ovarian cancer comprising providing to cells of the patient an antisense oligonucleotide complementary to a marker of the invention and a method of treating a marker in a markers are useful for assessing if a patient is afflicted with ovarian cancer comprising the level of expression of the invention. The marker is an excert and a normal level of expression of the marker in a patient sample and a normal level of expression of expression levels indicates ovarian cancer. The level of expression of a control non-ovarian cancer sample. A difference between the marker in a patient as of a secreted protein or to a transcribed polymucleotide or its portion. The level of expression of the marker is assessed by detecting the presence in the sample, a protein or protein fragment corresponding to the marker. The presence of protein or protein fragment. Alternatively, the level of expression of the marker is assessed by detecting the presence of a transcribed polymucleotide which anneals with the marker or anneals with a portion of the polymucleotide which anneals with the marker or anneals with a portion of sample at a first point in time, repeating the marker in a subsequent time and comparising the marker in a subsequent time and comparing the level of expression of the marker in a spatient which involves detecting expression. The method at a subsequent time and comparing the level of expression of the marker. The presence of a transcribed out using an ovarian tissue sample or a number of the marker or anneals with a
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Pred. No. 2.1e-09;
0; Mismatches 478;
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1447

Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.

WO200170979-A2 Homo sapiens

27-SEP-2001.

Human ovarian cancer DNA marker #21388.

(first entry)

20-MAY-2004

standard; DNA; 2318

ADL63176 ADL63176; 474

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2000US-0191637P.
2000US-00614150.
                                                                                          Claim 1; SEQ
 23-MAR-2000;
11-JUL-2000;
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                     GAAGAAGAAAACCAAGAGGCCACAGGCAGCCAAGGAAGCCGAGAAAGGGCCGCGCGAGGA
                                  biology; cell signalling; insecticide;
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                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher elacaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABBS777-BBS7272). The sequence data for this patent did not form part of printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                detection reagent for detecting 1000 or more for elucidating cell signaling and cell-cell
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46.9%; Pred. No. 2.3e-09;
iive 0; Mismatches 422; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3662 BP; 661 A; 941 C; 421 G; 1639 T; 0 U; 0 Other;
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genes from Drosophila and
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of cytosine methylation described in the

Sequence 1200 BP; 0 A; 112 C; 153 G; 919 T; 0 U; 16 Other;

disclosure of the invention for determining the degree

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                                                                                         Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons
                                                     1251 CGGACCGGACGAGGCCCCAAACACCAAGGAAAACAGAAAAGCCCGGGGGCACGAACA
                                                                                                                                                                                                                                              Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
                                                                                                                                                                                                                             Oligonucleotide for detecting cytosine methylation SEQ ID NO 25801.
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05-SEP-2000; 2000DE-01044543.
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from chemically treated DNA.
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                          776 CAAAAAGACCACCCCCAAACACAGAGGAGAAGGAGAACACCAGGAAGCCAAAGGAAAGG
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6.6%; Score 88.6; DB 6;
43.8%; Pred. No. 2e-09;
live 0; Mismatches 447;
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(first entry)

12-JUL-2002

This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member of oligonacieotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used:

(i) for diagnosis and/or prognosis of side effects of therspeutic drugs

German.

and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc.) particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously. ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the method

(i) for and of

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Oligonucleotide for detecting cytosine methylation SEQ ID NO 25802
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Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.

Homo

WO200218632-A2.

07-MAR-2002

01~SEP-2001; 2001WO-EP010074.

01-SEP-2000; 2000DE-01043826. 05-SEP-2000; 2000DE-01044543.

(EPIG-) EPIGENOMICS AG

Guetig Berlin K, Piepenbrock C, Ŕ

Ä

WPI; 2002-371829/40.

Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA.

Claim 12; 56pp + Sequence Listing; 56pp; German.

This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligoners and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used and of a wide range of diseases, e.g. cancer, disorders of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc. particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue types and for status of many C residues to be determined simultaneously. ABQ14410-ABQ54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the the invention

Sequence 1200 BP; 919 A; 153 C; 112 G; 0 T; 0 U; 16 Other;

536 AAGAAGAAAACCAAGAAGGCCACAGGGCAGCCAAGGAAGCCGGAGAAAGGGCCGCGAGAG Gaps ö Length 1200; 447; Indels 6; DB 6; 2e-09; 0; Mismatches Score 88.6; Pred. No. 2e 6.6%; al Similarity 43.8%; 349; Conservative Query Match 셤 Š

CGAAGACCGCCAGAGCCCAAAAGCCCAAGAAAGACACGGGACGAGGAAACCCA 296 959

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716 ACCAACAGGCCGAGACCGAGGCACCGGGCCGAGAGAGAACACCCACACGCCGAAGCCA

GCAGAGAAAAAGGCCCCAGGGCGAGGGCCAAGGCAAAGGAGAACCCCAAAGGAACGGAC 1255 CGGACGAGGCCCCAAACACCAAAGAAACAGAAAAAGCCCGCGCGCACGAACAGACCA 1315 1075 1015 911 731 851 CAAAAAGACCACCCCCAAACACAGAGGAGAAGGAGAACACCCAGGAAGCCAAAGGAAGAGG ACAACAGGGGGAGGGGGGGGGCGGCCGCCACAGAAGGAGAAAAAGCAGGAGAG 956 GCCAGACAAAGCAAAAGAAGCAGGCGAAACGGGCGAACACACAGAACAAAGAACGGCAGGA 612 лавававававававававававававававассвавававававававававав 1316 CACACAGCAGAGAAGA 1331 972 AAAAAAAAAAAAAAA 1076 732 1256 1136 1196 g 셤 g à g ð g ð ð 5 g à 셤 ð 셤 à

Search completed: October 21, 2004, 04:14:57 Job time : 739 secs

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Sequence 14, Appli
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Sequence 8286, Ap
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Compugen Ltd.
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US-08-91-99-4
US-08-91-99-4
US-09-270-767-8286
US-09-270-767-1308
US-09-270-767-1308
US-09-270-767-1308
US-09-270-767-1308
US-09-378-33-3
US-08-58-136-2
US-08-658-136-2
US-08-658-136-2
US-09-270-767-2034
US-09-270-767-2037
                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                      824507 seqs, 355394441 residues
                                                                                                                          US-10-019-341-4_COPY_256_1599
GenCore version (c) 1993 - 2004
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                                              OM nucleic - nucleic search, using sw model
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                             Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Sequence 1, Appli Sequence 4464, Ap Sequence 19746, A Sequence 13735, A Sequence 63, Appli Sequence 53, Appli Sequence 583, Appli Sequence 3, Appli Sequence 3, Appli Sequence 185, Appli Sequence 186, Appli Sequence 1, Appli Sequence 11, Appli Sequence 11866, Appli		
28 55.8 4.2 319608 4 US-09-679-409-1  29 55.6 4.1 936 4 US-09-270-767-4464  31 55.6 4.1 936 4 US-09-270-767-19746  32 54.2 4.0 168174 4 US-09-019-055A-13735  33 54.2 4.0 168174 4 US-109-11A-63  34 54.2 4.0 168273 4 US-109-11A-63  35 53.8 4.0 4453 3 US-09-128-352-583  36 53.8 4.0 4453 3 US-09-128-352-583  37 53.6 4.0 202001 4 US-09-328-352-585  40 53 3.9 447 4 US-09-328-352-585  41 52.6 3.9 668 1 US-08-316-552-68  42 52.6 3.9 668 4 US-09-050-314-1  43 51.8 3.9 6158 4 US-09-050-314-1  44 51.6 3.8 336 4 US-09-548-176-87  51.4 3.8 336 4 US-09-248-796A-13866  45 51.4 3.8 336 4 US-09-509-7128-4	ALIGNMENTS	RESULT 1  US-08-232-463-14/C    Sequence 14, Application US/08232463   Patent No. 5670367   TITLE OF INVENTION: RECOMBINANT FOWLDOX VIRUS   NUMBER OF SEQUENCES: 52   CORRESPONDENCE DADRESS: 52   ADDRESSEB: Folcy Lardner STREET: 1800 biagonal Road, Suite 500   CITY: Alexandria Alexandria STREET: 4A Alexandria STREET: 1800 biagonal Road, Suite 500   CITY: Alexandria Proper Sequences: 52013-0299   COMPUTER READABLE FORM: PC Compatible COMPUTER: IBM PC Compatible COMPUTER: Batentin Release #1.0, Version #1.25   COMPUTER: Patentin Release #1.0, Version #1.25   COMPUTER: Patentin Release #1.0, Version #1.25   COMPUTER: DATE: Batentin Release #1.0, Version #1.25   PRION APPLICATION NUMBER: US/07/935,313 FILING DATE: APPLICATION NUMBER: US/07/935,313 FILING DATE: APPLICATION NUMBER: EP 91 114 300.6   FILING DATE: APPLICATION NUMBER: BS 91 114 300.6   REFERENCE CHARCITERISTICS: APPLICATION NUMBER: S0.768     RESISTANTION POR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS: LENGTH: TYPE : nucleic acid of TYPE: Nucleic acid of Nucleic acid of TYPE: Nucleic acid of Nuc

Length 7218;

DB 1;

9.6%; Score 129.6;

Query Match

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947 CGGAGGAAAGCCAGACAAGCCGAAAAGAAGCAGGCGAAACGGGGAACACAGAACAAAGA 1006
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                                                                                                                       11;
                                                                                               Length 6755;
                                                                                            Score 102; DB 3; Length 67
Pred. No. 9.1e-14;
0; Mismatches 675; Indels
                                             : Staphylococcus aureus
UT0007
DNA (genomic)
                                                                                                  7.6%;
                                                                                                  Query Match
Best Local Similarity 45.3
Matches 568; Conservative
           HYPOTHETICAL: N
ANTI-SENSE: NO
ORIGINAL SOURCE:
MOLECULE TYPE:
                                                 ORGANISM:
                                                              STRAIN:
US-08-931-999-4
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                                                                                       Gaps
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APPLICANT: Crupper, Scott S.
IIILE OF INVENTION: Broad Spectrum Chemotherapeutic Peptide
               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Version #1.30
               83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSEE: Hovey, Williams, Timmons & Collins F: 2405 Grand Boulevard, Suite 400 Kansas City
     No. 6.1e-20
     Best Local Similarity 1.6%; Pred. No. 6.1e-
Matches 6; Conservative 289; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/710,561
FILING DATE: 19-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/931,999
                                                                                                                                                                                                                                                                                                                                                              REPREKER REPART 1059
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/08931999
Patent No. 6043219
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                             1230 CAAAGGAGAACCCCAAAG 1247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Collins, John M.
REGISTRATION NUMBER: 26,3
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          816/474-9050
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Missouri COUNTRY: U.S.A. ZIP: 64108 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Hovey, Wi
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US-08-931-999-4
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TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: FILE REFERENCE: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SEQ TO NO 23568
LENGTH: 851
                                                     GACCCGGAAGAAAACCAAGAAGGCCACAGGGCAGCCAAGGAAGCCGAGAAAGGGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          769 GAAGCCACAAAAAGACCACCCCCAAACACAGAGGAGAAGGAGAACACCCAGGAAGCCAA-A
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Pred. No. 1e-09;
); Mismatches 357; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: n means any nucleotide US-09-270-767-23568
                                                                                                                                                                                                                                                     US-09-270-767-23568/c
; Sequence 23568, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
                                                                                                                                                                                              1188 AAAGGAGCGCAGAGAAAAAGG 1209
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Best Local Similarity 47.1<sup>§</sup>
Matches 321, Conservative
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US-09-270-767-8286/c

Sequence 8286, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:

APPLICANT: Homburger et al.

ATILE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

TILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFWARE: Patentin Ver. 2.0
                                                                                       1187 AAAAGGAGCGCAGAGAAAAAGGCCCCAGGGCGAGGGCCAAGGCAAAGGAGAAACCCCAAA
                                                                                                                                                                      6547 GAGAACAGAAAACAAGAGGAACAACAAAGAAAGGGGAGGCAAAAGAACAAAA
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llarity 47.1%; Pred. No. 1e-0
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: n means any nucleotide US-09-270-767-8286
                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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Best Local S:
Matches 321
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Pred. No. 1.4e-09;
0; Mismatches 334;
                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of
TITLE OF INVENTION: Nucleic acids and proteins of
TITLE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 16590
LENGTH: 1827
                                                                                                                                                                                                                                                                       Sequence 16590, Application US/09270767 Patent No. 6703491
                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-16590
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 48.4%;
Matches 320; Conservative
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US-09-270-767-16590
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                                                                                                                                                                                          APPLICANT: Homburger et al.
TILLE OP INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT FILLNG NUMBER: US/09/270,767
NUMBER OF SEQ ID NOS: 1999-03-17
SOFTWARE: PATENTIN OS: 25517
SOFTWARE: PATENTIN US: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAGAGACCAGAAAAAGGGACCGCAGGAAAAGGCCAGCAGAAAGGAAAGGCACCGCGGA
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GGAAGAAGAAACCAAGAAGGCCACAGGCAGCCAAGGAAGCCCGAAAAGGGCCGCGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4;
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Pred. No. 1.4e-09;
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Patent No. 6703491
GENERAL INFORMATION:
                                                                                                                                                                                                                                         167 TGGGGGGGGGGAGGGGGG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ), ORGANISM: Drosophila melanogaster US-09-270-767-1308
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Best Local Similarity 48.4%;
Matches 320; Conservative
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US-09-270-767-1308
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Sequence 3 Application US/09510543

| Sequence 3 Application US/09510543
| Patent No. 6517837
| GENERAL INFORMATION:
| APPLICANT: Scanlan, Matthew J.
| APPLICANT: Stockert, Elisabeth
| APPLICANT: Chen, Yao-Teeng
| APPLICANT: Old, Lloyd J.
| TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ASSOCIATED WITH COLON CANCER AND TITLE OF INVENTION: METHODS FOR DIAGNOSING AND TREATING COLON CANCER ITILE OF INVENTION: METHODS FOR DIAGNOSING AND TREATING COLON CANCER STILLS REFERENCE: LUD-5566.1-05L/NDH
| TITLE OF INVENTION: METHODS FOR DIAGNOSING AND TREATING COLON CANCER STILLS REPERENCE: LUD-5566.1-05L/NDH
| TITLE OF INVENTION: METHODS FOR DIAGNOSING AND TREATING COLON CANCER AND STILLS PRIOR APPLICATION NUMBER: US/09/510,543
| PRIOR APPLICATION NUMBER: US 09/102,322
| PRIOR FILING DATE: 1998-06-22
| NUMBER OF SEQ ID NOS: 22
| SEQ ID NO 3
| LENGTH: 1298
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                                                                                                                                                                                      5.3%; Score 70.8; DB 3; 149.0%; Pred. No. 5.5e-07; tive 0; Mismatches 246;
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Matches 242; Conservative
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ORGANISM: Homo sapiens
                      NAME/KEY: unsure
LOCATION: 1101..1101
OTHER INFORMATION:
                                                                                                ; NAME/KEY: unsure
; LOCATION: 1144..1144
; OTHER INFORMATION:
US-08-948-705-3
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Batent No. 6643084
GENERAL INFORMATION:
APPLICANT: Scanlan, Matthew J.
APPLICANT: Chen, Yao-Tseng
APPLICANT: Old, Lloyd J.
TITLE OF INVENTION: ASSOCIATED WITH COLON CANCER AND METHODS FOR DIAGNOSING AND
TITLE OF INVENTION: TREATING COLON CANCER
FILE REFERENCE: LUD-5506-JEL/NDH
CURRENT APPLICATION NUMBER: US/08/948,705A
CURRENT APPLICANTON 1997-10-10
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                   1130
TYPE: DNA
ORGANISM: Homo Sapiens
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LOCATION: 1058..1058
OTHER INFORMATION:
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OTHER INFORMATION:
FEATURE:
NAME/KEY: unsure
LOCATION: 141..141
OTHER INFORMATION:
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NAME/KEY: ungure
LOCATION: 750..750
OTHER INFORMATION;
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NAME/KEY: unsure
LOCATION: 722..722
OTHER INFORMATION:
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NAME/KEY: unsure
LOCATION: 199..99
OTHER INFORMATION:
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LOCATION: 342..342
OTHER INFORMATION:
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LOCATION: 352..352
OTHER INFORMATION:
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GENERAL INCORMATION:

GENERAL INCORMATION:

APPLICANT: ABU-THREIDEH, Jane et al

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: THEREOF

FILE REFERENCE: CLOOLO43

CURRENT APPLICATION NUMBER: US/10/207,973

CURRENT FILING DATE: 2002-07-31

NUMBER OF SEQ ID NOS: 3

SOFTWARE: PASESEQ for Windows Version 4.0

SEQ ID NO 9591
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| Sequence 3, Application US/09759359A
| Patent No. 6422153
| Patent No. 642
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Pred. No. 1.2e-05;
0; Mismatches 223;
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Patent No. 6753175
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ORGANISM: Human
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Pred. No. 5.5e-07;
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COCATION: 1101.1101
CTHER INFORMATION:
NAME/KEY: unsure
COCATION: 1144.1144
CTHER INFORMATION:
US-09-510-543-3
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OTHER INFORMATION:
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NAME/KEY: unsure
LOCATION: 750..750
OTHER INFORMATION:
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NAME/KEY: unsure
LOCATION: 352..352
OTHER INFORMATION:
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OTHER INFORMATION:
NAME/KEY: unsure
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OTHER INFORMATION:
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OTHER INFORMATION:
                                                                                  LOCATION: 141..141
OTHER INFORMATION:
NAME/KEY: unsure
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LOCATION: 722..7
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Best Local Simi
Matches 242;
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REGISTRATION NUMBER:
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                                     Length 90541;
                                   Score 67.2; DB 4; Length 9
Pred. No. 1.2e-05;
0; Mismatches 223; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,136
                                                                                                                                                                                                                                                                                                                                   34691 ACGGAAGGAAGAAGAAATCAGC 34666
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: GENZYME CORPORATION ONE MOUNTAIN ROAD
                                                                                                                                                                                                                                                                                                                                                            RESULT 11
US-08-658-136-2/c
Sequence 2, Application US/08658136;
Patent No. 6071717;
GENERAL INFORMATION:
APPLICANT: KATHERINE W
TANNER CAPEGORY M
                                                                                                                                                                                                                                                                                                                                                                                                               LANDES, GREGORY M
BURN, TIMOTHY C
CONNORS, TIMOTHY D
DACKOWSKI, WILLIAM
GERMINO, GREGORY
                                   Query Match 5.0%;
Best Local Similarity 48.7%;
Matches 217; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LASSEN, ELIZABETH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MASSACHUSETTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: FRAMINGHAM
; TYPE: DNA
; ORGANISM: Human
US-10-207-973-3
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                 Score 63.8; DB 3; ]
Pred. No. 5.8e-05;
0; Mismatches 557;
REFERENCE/DOCKET NUMBER: GEI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 508-872-8400
TELEFAK: 508-872-5415
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                         ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-658-136-2
                                                                                                                                                                                 Query Match
Best Local Similarity 45.8%;
Matches 491; Conservative (
                                                                                  : 53526 base pairs
nucleic acid
                                                                                                         STRANDEDNESS: single
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US-09-270-767-5061
US-09-270-767-5061
; Sequence 5061, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
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                                         GGGGACAGGGGGCCCGGACAACGGAGGAGGAGAACACCCCCGGACAAGCCACCGGGA
                  GAACACAAAACAACCCAGGGGGGGGCAAAAGGGAACCGAAAAACCCAGCCCACCCGAGAAGG
                                                                                             AGAC - - AGCCAAGCACAAAAAGGGCAACAAAGGGGAAAGGGCCAAAAAGCACACCCCAACGA
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                                                                                                                                                                                                                                                                                                            APPLICANT: LANDES, GREGORY M
APPLICANT: BURN, TIMOTHY C
APPLICANT: CONNORS, TIMOTHY C
CONNORS, TIMOTHY D
APPLICANT: GACKOWSKI, WILLIAM
APPLICANT: GENAINO, GREGORY
APPLICANT: GAN FENG
TITLE OP INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
AURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,136
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENZYME CORPORATION
                                                                                                                                                                                                                                                           Sequence 1, Application US/08658136
Patent No. 6071717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: LASSEN, ELIZABETH
REGISTRATION NUMBER: 31,845
REFERENCE/POCKET NUMBER: GEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 508-872-8400
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MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
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Best Local Similarity 45.8%;
Matches 491; Conservative
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MASSACHUSETTS
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US-08-658-136-1/c
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COUNTRY:
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US-08-658-136-1
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                                                                                                                                                                                                                                                                                                                              GCAGGGAGAAAGGCCAGCAGAAAGGAAAGGCACCGCGGAG-GAAAGCCAGACAAGCCGAA 970
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20143, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PATENTIN VET. 2.0
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5061
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Pred. No. 1.9e-05;
0; Mismatches 214; Indels
                                                                                                                                                                                     Length 705;
                                                                                                                                                                                     Score 63.6; DB 4; Length 7
Pred. No. 1.9e-05;
0; Mismatches 214; Indels
                                                                                                                             ; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-5061
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Best Local Similarity 48.6%;
Matches 203; Conservative
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Best Local Similarity 48.6%;
Matches 203; Conservative
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US-09-270-767-20343
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LENGTH: 705
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Batent No. 5614694

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Milhausen, Michael James
TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND USES:
FILE REPERENCE: TX.1-C2
CURRENT APPLICATION NUMBER: US/09/216,393B

PRIOR PILING DATE: 1998-12-18
PRIOR FILING DATE: 1997-12-19

NUMBER OF SEQ ID NOS: 366
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                         GCAGGGAGAAAGGCCAGCAGAAAGGAAAGGCACCGCGGAG-GAAAGCCAGACAAGCCGAA
                                                                        GACCGCCAGAGCCCACAAAGCCCAACCAAGAAAGACACGGGACGAGGAAAACCCAACCA
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Pred. No. 2.5e-05;
0; Mismatches 404;
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ilarity 47.6%;
Conservative
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OTHER INFORMATION:
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Best Local Simi
Matches 377;
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957 CCAGACAAGCCGAAAAGAAGCAGGCGAAACGGGCGAACACAGAACAAAGAACGGCAGGAA 1016
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                                                             900 GAAAAAAGGGACCGCAGGAAGAAAGGCCCAGCAGA---AAGGAAAGGCACCGCGAAGAAAG 956
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Search completed: October 21, 2004, 07:12:04 job time : 143 secs

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Sequence 17, Appl
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Sequence 21388, A
Sequence 39710, A
Sequence 2359, Ap
Sequence 2003, Ap
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                                                                                                                                                                                                                                                                                                                                                   Description
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-814-353-21388
US-10-369-493-39710
US-10-017-161-2359
US-10-022-798-2003
US-10-004-113-43
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US-10-125-767-17
US-10-151-081-17
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Match Length DB
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Sequence 1670, Ap Sequence 70, Appl Sequence 71, Appl	Sequence 12701, A Sequence 39721, A	Sequence 168583, Sequence 168584,	Sequence 168585, Sequence 168586,	Sequence 168583,	Sequence 168584,	Sequence 168585,	Sequence 14764, A	Sequence 42302, A	Sequence 17, Appl	Sequence 2113, Ap	Sequence 1759, Ap	Sequence 2299, Ap	Sequence 1945, Ap	Sequence 10433, A	Sequence 2020, Ap	Sequence 64, Appl	45,	219	183	397	721	817,		210	-	
US-10-311-455-1670 US-10-001-843-70 US-10-001-843-71	US-10-198-846-12701 US-10-369-493-39721	US-10-027-632-168583 US-10-027-632-168584	US-10-027-632-168585 US-10-027-632-168586	US-10-027-632-168583	US-10-027-632-168584	US-10-027-632-168585 US-10-027-632-168586	US-09-814-353-14764	US-10-437-963-42302	US-10-001-857-17	US-10-017-161-2113	US-10-292-798-1759	US-10-017-161-2299	US-10-292-798-1945	US-10-198-846-10433	US-10-087-192-2020	US-10-331-053-64	US-10-001-843-45	US-10-017-161-2193	US-10-292-798-1839	US-10-369-493-39722	US-10-437-963-72176	US-09-834-975-817	US-10-021-323-9336	US-10-017-161-2107	US-10-292-798-1753	
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## ALIGNMENTS

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RESULT 1

US-09-7994-462A-17/C

US-08-7994-62A,

Patent No. US20020160970A1

Sequence 17, Application US/09799462A

Patent No. US20020160970A1

GENERAL INFORMATION:

APPLICANT: Hadlaczky, Gyula

APPLICANT: Hadlaczky, Gyula

TITLE OF INVENTION: ARTIFFICIAL CHROMOSOMES, USES THEREOF

TITLE OF INVENTIONS: 34

CORESPONDENCE ADDRESS:

CRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRESS:

COMPUTR: La Jolla

STATE: CA

COMPUTR: La Jolla

STATE: CA

COMPUTR: LB COMpatible

COMPUTR: LB COMPATION: -CURINOWN-

PRILICATION NUMBER: 08/09/799, 462A

FILING DATE: 10-APR-1997

APPLICATION NUMBER: 08/635, 682

FILING DATE: 10-APR-1996

APPLICATION NUMBER: 08/629, 822

APPLICATION NUMBER: 08/629, 822

ATTORIEY ADDRESS: 10-APR-1996

ATTORIEY ADDRESS: 10-APR-1996
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24979

1106

1166

24926

1223

25099

986

1046

25039

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1224 CCAAGCCAAAGGAGAACCCCAAAGGAACGGACCGGACGAGGCCC---CAAACACCAAGCC 1280
APPLICANT: Hadlaczky, Gyula
Szalay, Aladar
TITLE OF INVENTION: ARTIFICIAL CHROWOSOMES, USES THEREOF
AND METHODS FOR PREPARING ARTIFICIAL CHROMOSOMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25158 AGACAGACAGACAGACAGACAGGAGGAGGAGGAGTAAGACAAAAAGATACACAGAGA
                                                                                                                                                                                      1107 CACAAAAAGGGCAACAAAGGGGGAAGGGCCAAAAAGCACACCCCAACGAAAAGACAGGGACA
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                           ADDRESSEE: Heller Ehrman White & McAuliffe
STREET: 4350 La Jolla Village Drive, 6th Floor
CITY: San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FRAESEQ VErsion 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/836,911A
FILING DATE: 17-APP-2002
CLASSIFCATION: CURLOWN>
PRIOR APPLICATION NUMBER: 08/835,682
APPLICATION NUMBER: 08/835,682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 10-APR-1997
APPLICATION NUMBER: 08/695,191
FILING DATE: 07-AUG-1996
APPLICATION NUMBER: 08/682,080
FILING DATE: 15-UUL-1996
APPLICATION NUMBER: 08/629,822
FILING DATE: 10-ARR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-836-911A-17/c; Sequence 17, Application US/09836911A; Publication No. US20030033617A1
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CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                             Score 94.8; DB 9;
Pred. No. 2.1e-12;
0; Mismatches 655;
 NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24601-402G
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                 FRAGMENT TYPE: «Unknown»

ORIGINAL SOURCE:
US-09-799-462A-17
                                                                                 INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 42999 base pairs
TYPE: nucleic acid
                                                             TELEPHONE: 858-450-8403
TELEFAX: 858-587-5360
                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: Genomic DNA
                                                                                                                                                                      STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                             Query Match 7.1%;
Best Local Similarity 45.3%;
Matches 568; Conservative
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APPLICANT: Greenspan, Ralph J.
APPLICANT: Graw, Paul J.
TITLE CANTENTION: Mehtods For Identifying Compounds That
TITLE OF INVENTION: Modulate Disorders Related To Nitric Oxide/cGMP-Dependent
TITLE OF INVENTION: Protein Kinase Signaling
FILE REFERENCE: P-NI 3906
CURRENT APPLICATION NUMBER: US/09/738,630
CURRENT FILING DATE: 2000-12-15
SOFTWARE FILING DATE: 2000-12-15
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                             24865 ACAGACAGAGAGACACAGAAAAAGAAAGAGGGGGCAGACAGACAGAGAAAGAGAGAT 24806
                                                                                                                                                                                                                                          1224 CCAAGCCAAAGGAGAACCCCAAAGGAACGGACCGGACGAGGCCC---CAAACACCAAGCC 1280
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        24805 AGAGAAAGAGAGAGAGAGAGAGAGAGAGAAACAGAAAAGAGAGAGAGAGA 24751
                                                                                                                                                                                                                                                                                                                                                                                                   CACAAAAAGGGCAACAAAGGGGAAGGGCCAAAAGCACCCCCAACGAAAAGACAGGGACA
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                                          25262 AGACAGACAGAGAAAGGGACAGACAGAGAAAGACAGAGACAGAGAGAGAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 73, Application US/09738630; Publication No. US20030166213A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature
LOCATION: (1)...(42999)
OTHER INFORMATION: n = A,T,C or
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ORGANISM: Homo sapiens
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NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24601-4021
TELECOMPULCATION INFORMATION:
TELEPHONE: 858-450-8403
TELEFRAX: 858-587-5360
                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-836-911A-17
                                                                                                                                  ORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
TYPE: nucleic acid
STRANDEDENESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
                                                                                                                                                                                                                                                                                                                 FRAGMENT TYPE: <Unknown>
                                                                                                                    TELEX: <Unknown>
                                                                                                                                                                                                                                                                           HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                             ANTI-SENSE: NO
                                                                                                                                      INFORMATION FOR
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COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ Version 1.5
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TELEFAX: 858-587-5360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                         ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DESCRIPTION: SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <Unknown>
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Best Local Similarity 45.3
Matches 568; Conservative
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                                                       RESULT 4
US-10-125-767-17/c
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                                                                             AAGAAAGACACGGGACGAGAGGAAACCCAACAACAGGCCGAGACGGAGGCACCGGGCCG
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            GGGCCCGGACACGGAGGAGGAGAACACCCCGGACAAGCCACCGGAACAGCCGGGAG
                                                        CCCAG----CGCGGCAGCAAGGAAGCAAAAGAAAGCAACAGAAACGGCCCGACCAGCG
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                                           24805 AGAGAAAGAGAGAGAGACAGAGAGAGACAGAAACAGAAAAGAAAAGAGAGAGAGA 24751
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1281 CAAGAAACAGAAAAGCCCGCGCGCACGAACAGACCACACACAGAGAGAGAGA
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                                                                                                                                                                                                                                                                                                      FOR PREPARING ARTIFICIAL CHROMOSOMES
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                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADORESSEE: Heller Bhrman White & McAuliffe LLP
STREET: 4350 La Jolla Village Drive, 7th Floor
CITY: San Diego
STATE: CA
                                                                                                                                                                                                                                                           USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 94.8; DB 13;
Pred. No. 2.1e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 2.1e-12;
0; Mismatches 655;
                                                                                                                                                              Sequence 17, Application US/10125767
Publication No. US20020160410A1
GENERAL INFORMATION:
APPLICANT: Hadlaczky, Gyula
TITLE OF INVENTION: ARTIFICIAL CHROMOSOMES,
METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24601-402J
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/10/125,767 FILING DATE: 17-Apr-2002 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 09/724,693
PILING DATE: 28-NOV-2000
APPLICATION NUMBER: 08/695,682
FILING DATE: 10-APR-1997
APPLICATION NUMBER: 08/695,191
FILING DATE: 10-ADG-1996
APPLICATION NUMBER: 08/69,080
FILING DATE: 15-JUL-1996
APPLICATION NUMBER: 08/629,822
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ID NO: 17:
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ARTIFICIAL CHROMOSOMES, USES THEREOF
AND METHODS FOR PREPARING ARTIFICIAL CHROMOSOMES
                                                             24805 AGAGAAAGAGAGAGCAGACAGAGAGACAGAAAGAGAAAGAGAGAGAGA 24751
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                                1281 CAAGAAACAGAAAAGCCCGCGGCACGAACAGACCACACACACAGAGAGAGAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32;
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                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Ehrman White & McAuliffe
STREET: 4250 Executive Square, 7th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; DB 14;
2.1e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 33,779
REFERENCE/BOCKET NUMBER: 24601-402L
TELECOMUNICATION INFORMATION:
TELEPHONE: 858-450-8403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: HEREWITH 05-MAR-2001
APPLICATION NUMBER: 09/724,693
FILING DATE: HEREWITH 28-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/10/151,081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/835,682
FILING DATE: 10-APR-1997
APPLICATION NUMBER: 08/695,191
FILING DATE: 07-AUG-1996
APPLICATION NUMBER: 08/682,080
FILING DATE: 15-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 94.8;
Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 09/799,462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/629,822
FILING DATE: 10-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DESCRIPTION: SEQ ID NO: 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Seidman, Stephanie L
                                                                                                                                                                                                                                                                   TITLE OF INVENTION: ARTIFICIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 16-May-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                   Sequence 17, Application US/10151081
Publication No. US2003008329331
GENERAL INFORMATION:
APPLICANT: Hadlaczky, Gyula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 42999 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 858-587-5360
TELEX: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: Genomic DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 92037
COMPUTER READABLE FORM
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Matches 568; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                        STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: <Un
ORIGINAL SOURCE:
SEQUENCE DESCRIPTI
                                                                                                                                              US-10-151-081-17/c
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25922 ACAGACAGAGAAAGACAGAGACAGACAGAGAAACAGGCAGAAAGAGAGAGAGAGAGAGAG 25863
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                                                                             CCCAG----CGCGGCAGCAGGAAGCGACCAAAAGAAAGCAACAGAAACGGCCCGACCAGCG
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TELECOMMUNICATION INFORMATION:
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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TYPE: nucleic acid
                                                                                                                                                                     Sequence 17, Application US/10287313
Publication No. US20030101480A1
GENERAL INFORMATION:
APPLICANT: Hadlaczky, Gyula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 858-450-8403
TELEFAX: 858-587-5360
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MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 45.3%;
Matches 568; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <Unknown>
                                                                                                                                                                                                                                                                                                                                                                         ZIP: 92037
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
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                                                                                      210 GGGCCCGGACAACGGAGGAGGAGAAAACACCCCGGACAAGCCAACGGGAAACAGCCGGAG
                                                                                                                                            GACCAACGAGAGCAGAGCCCCCGAGCGCCCCGAGAGCAGAGACGCACACACACACACAC
                                                                                                                                                                                                                                                            25682 AAGAGAAAACAGGCAGAGAGAGAGAGAGCTAGCGAGAGAAACAAAAAGGTAGGGAGA
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CCAAGCCAAAGGAGAACCCCAAAGGAACGGACCGGACGAGGCCC---CAAACACCCAAGCC 1280
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TITLE OF INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF
AND METHODS FOR PREPARING ARTIFICIAL CHROMOSOMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                               Length 42999,
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                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Ehrman White & McAuliffe
STREET: 4250 Executive Square, 7th Floor
CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/287,313
FILING DATE: 01-NO. US20030101480A1-2002
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION NUMBER: 09/724,726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 94.8; DB 15;
Pred. No. 2.1e-12;
0; Mismatches 655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6869-402N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 28-NOV-2000
APPLICATION NUMBER: 08/835,682
FILING DATE: 10-APR-1997
APPLICATION NUMBER: 08/695,191
FILING DATE: 07-AUG-1996
APPLICATION NUMBER: 08/682,080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DESCRIPTION: SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 15-JUL-1996
APPLICATION NUMBER: 08/629,822
FILING DATE: 10-APR-1996
ATTORNEY/AGENT INFORMATION:
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UDIICATION NO. COLONIE OF THE SELECTION:
GENERAL INFORMATION: HAGIACZKY, GYULA
TITLE OF INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF AND METHODS
FOR PREPARING ARTIFICIAL CHROMOSOMES
                                                 24805 AGAGAAAGAGAGAGAGACAGAGAGAGACAGAAACAGAGAAAGAGAGAGAGAGA 24751
                                                                             14865 ACAGACAGAGAGACACAGAAAAAAAAGAGAGGGCAGACAGACAGAAAAAGAGACAGAT
                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Ehrman White & McAuliffe LLP
STREET: 4350 La Jolla Village Drive, 7th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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Pred. No. 2.1e-12;
0; Mismatches 655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: «Unknown»
FILING DATE: 28-NOV-2000
APPLICATION NUMBER: 08/85,682
FILING DATE: 10-APR-1997
APPLICATION NUMBER: 08/695,191
FILING DATE: 07-ANG-1996
APPLICATION NUMBER: 08/692,080
FILING DATE: 15-UL-1996
APPLICATION NUMBER: 08/629,822
FILING DATE: 10-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Seldmania L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 33,779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/219,694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DESCRIPTION: SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 14-Aug-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                       Sequence 17, Application US/10219694
Publication No. US20030108914A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 42999 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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TELEFAX: 858-587-5360
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MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: NO
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INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
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FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEG
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Best Local Similarity 45.3%;
Matches 568; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 92122
COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                               CITY: San Diego
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                                                     150 GGGGACGGCGCACGGGCCAAGGACCAAGGCCGCGGGCACACCAAACGGGGGACAGA
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150 GGGGACGGCGCCAGGAGCAACCCAGGCCGCGGGCACACCCAAACGGGGACAGGA
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                                                                                                1224 CCAAGCCAAAGGAGAACCCCAAAGGAACGGACCGGACGAGGCCC---CAAACACCCAAGCC
                                              GENERAL INFOGRATION:

GENERAL INFOGRATION:

APPLICANT: Hadlaczky, Gyula

TITLE OF INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF AND

TITLE OF INVENTION: METHODS FOR PREPARING ARTIFICIAL CHROMOSOMES

FILE REFERENCE: 24601-40.29

CURRENT FILING DATE: 2000-11-28

PRIOR APPLICATION NUMBER: US/09/724,693

PRIOR APPLICATION NUMBER: US/09/724,693

PRIOR APPLICATION NUMBER: US/09/724,693

PRIOR PILING DATE: 1997-04-10

PRIOR FILING DATE: 1997-04-10

PRIOR PILING DATE: 1996-08-07

PRIOR FILING DATE: 1996-08-07
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OTHER INFORMATION: n = A,T,C or G
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Genbank Accession No.
DATABASE ENTRY DATE: 1997-01-07
                                                                                                                                                                                                                                                                                                                                                                            ; sequence 17, Application US/10808689; Publication No. US20040163147A1; GENERAL INFORMATION:
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COMPOSITIONS, KITS, AND METHODS ION, ASSESSMENT, PREVENTION, AND
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6.6%; Score 88.8; DB 10;
Best Local Similarity 47.1%; Pred. No. 4.5e-11;
Matches 435; Conservative 0; Mismatches 478;
     TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KIT TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, IN TITLE OF INVENTION: THERAPY OF OVARIAN CANCER FILE OF INVENTION: THERAPY OF OVARIAN CANCER CURRENT APPLICATION NUMBER: US/09/814,353 CURRENT FILING DATE: 2001.03-21 CURRENT FILING DATE: 2000-03-21 PRIOR APPLICATION NUMBER: US 60/191,031 PRIOR FILING DATE: 2000-05-25 PRIOR APPLICATION NUMBER: US 60/211,940 PRIOR FILING DATE: 2000-06-15 PRIOR FILING DATE: 2000-07-07 PRIOR FILING DATE: 2000-07-07 PRIOR FILING DATE: 2000-07-07 PRIOR FILING DATE: 2000-07-07 PRIOR APPLICATION NUMBER: US 60/257,672 PRIOR PRING DATE: 2000-07-25 PRIOR PRIOR PRING DATE: 2000-07-25 PRIOR P
                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 22037
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21388
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: LOCATION: 1, 2, 3, 4, 5, 6, 2221, 2318
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-21388
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AAGAGAGAAAACAGGCAGAGAGAGAGCTAGCGAGAGAGAAACAGAAAGGTAGGGAGA
                                                                                                          15622 GAGAGAGÁGACAGÁCAGACAGATGGACAGGCAGAGÁGÁGÁGÁGAGAGACAGÁGAG
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RESULT 9
US-09-814-353-21388
US-09-814-353-21388
Sequence 21388, Application US/09814353
Publication No. US20030165831A1
GENERAL INFORMATION:
APPLICANT: Lee, John
APPLICANT: Linompson, Pamela
APPLICANT: Linompson, Pamela

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                                                         AGACCACCCCCAAACACAGAGGAGAAGGAGAACACCCAGGAAGCCAAAGGAAGAGGACAAC
                                                                                    AAAAACAGAGAAACCAACAGCCCAAAATGACAGGAGAGAAAC----GGAACACAGC
                                                                                                                                                                                                                                                                        685 ACAAAACAGAGAAGAAGGACCAAGAAG-GAAAAGAAGCGAGAAAACAGAGCACATGA
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APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAMA, YUTARA
APPLICANT: ARIAMA, YUTARA
APPLICANT: ABURALANI, HIROYUKI
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
FILE REPRENCE: 084335/0152
CURRENT APPLICATION NUMBER: US/10/017,161
CURRENT PILING DATE: 2002-02-18
PRIOR PILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2430
SOFTWARE: PALENTIN VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 2359, Application US/10017161; Publication No. US20030143668A1; GENERAL INFORMATION:
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LOCATION: (201)..(1640)
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US-10-017-161-2359/c
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ORGANISM: HOMO
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FEATURE:
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Stater, Steven C.
APPLICANT: Goldman, Barry C.
APPLICANT: Goldman, Barry C.
APPLICANT: Goldman, Barry C.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369, 493
CURRENT APPLICATION NUMBER: US 60/360, 039
PRIOR APPLICATION NUMBER: US 60/360, 039
                                                                                                                               1069 CCGAAAAACCCAGCCCACCGAGAAGGAGACAGCCAAGAGCACAAA---AAGGGCAACAAAG 1125
                                                                                                                                                                                                                       540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     210 AGAACAAAAACGCAACAAGCGGAATTCGCCGCAAAAACAAGTTTGCAAGAAAACGGAGAGA
                                                                                                                                                                                                                                                                            891 GAGAGA-CCAGAAAAAGGGACCGCAGGAGAAAGGCCAGCAGAAAGGAAAAGGCACCGCGG
                                                                    AGGAAAGCCAGACAAGCCGAAAAGAAGCAGGCGAAACGGGCGAACACAGAACAAAGAACG
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CTHER INFORMATION: unsure at all n locations
US-10-369-493-39710
                                                                                                                                                                                                                                                                                                                                                  AAGGAGGCACAAAGAGACAAGAG 2250
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 39710, Application US/10369493 Publication No. US20030233675A1 GENERAL INFORMATION:
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ORGANISM: Xanthomonas campestris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tch 6.6%; al Similarity 47.0%; 404; Conservative
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Matches 404; Conserva
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LENGTH: 1468
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g, unknown or other
                                                                                                                                                                   c, g, unknown or other
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                                                                                                                                                                                                                                                                               LOCATION: (39)
OTHER INFORMATION: a, t, c, g, unknown or other
                                                                                                 g, unknown or other
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LOCATION: (98)..(99)
THER INFORMATION: a, t, c, g, unknown or other
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CCCATION: (110)..(112)
THER INFORMATION: a, t, c, g, unknown or other
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NAME/KEY: modified_base
LOCATION: (126)
OTHER INFORMATION: a, t, c, g,
FEATURE:
NAME/KEY: modified_base
LOCATION: (130)
OTHER INFORMATION: a, t, c, g,
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LOCATION: (143)
DIHER INFORMATION: a, t, c,
                          OTHER INFORMATION: a, t, c
FEATURE:
NAME/KEY: modified base
LOCATION: (12)
OTHER INFORMATION: a, t, c
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INFORMATION: a, t,
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OTHER INFORMATION: a, t,
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THER INFORMATION: a, t,
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NAME/KEY: modified_base
modified_base
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NAME/KEY: modified_base
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SOCATION: (120)
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NAMESTER: modified_base
LOCATION: (150)
OTHER INFORMATION: a, t, c, g, unknown or other
NAME/KEY: modified base
LOCATION: (146)..(148)
THER INFORMATION: a, t, c, g, unknown or other
FEATURE:
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NAME/KEY: modified base
LOCATION: (161)..(162)
OTHER INFORMATION: a, t, c, g, unknown or other
                                                                                                                                                                                       g, unknown or other
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OTHER INFORMATION: a, t, c, g, unknown or other
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NAME/KEY: modified_base
LOCATION: (182)
OTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (186)
OTHER INFORMATION: a, t, c, g, unknown or other
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NAME/KEY: modified base
LOCATION: (192)..(194)
OTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (189)
THER INFORMATION: a, t, c, g, unknown or other
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NAME/KEY: modified base
LOCATION: (241).. (242)
OTHER INFORMATION: a, t, c, g, unknown or other
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NAME/KEY: modified_base
LOCATION: (249)
OTHER INFORMATION: a, t, c, g, unknown or other
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OTHER INFORMATION: a, t, c, g, unknown or other
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INFORMATION: a, t, c, g, unknown or other
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OTHER INFORMATION: a, t, c, g, unknown or other
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NAME/KEY: modified_base
LOCATION: (152)
OTHER_INFORMATION: a, t, c,
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NAME/KEY: modified base
LOCATION: (155)..(156)
OTHER INFORMATION: a, t, c,
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LOCATION: (235)
OTHER INFORMATION: a, t, c,
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NAME/KEY: modified_base
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NAME/KEY: modified_base
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Sequence 2003, Application US/10292798
; Sequence 2003, Application US/10292798
; bublication No. US20030235833A1
; GENERAL INFORMATION:
; APPLICANT: SUMA, MAZIKO
; APPLICANT: ASMA, WITAKA
; APPLICANT: ASMA, MITACOUNI
; APPLICANT: ASMA, MITACOUNI
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 084335/166
; CURRENT APPLICATION NUMBER: US/10/292,798
; FILE REPERENCE: 2001-13
; PRIOR PELICATION NUMBER: 10/017,161
; PRIOR FILING DATE: 2001-246789
; PRIOR FILING DATE: 2001-06-18
; PRIOR PELICATION NUMBER: JP 2001-246789
; PRIOR PELING DATE: 2001-06-18
; SOFTWARE: PatentIN Ver. 2.1
; SEQ ID NO 2003
; LENGTH: 1840
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OTHER INFORMATION: a, t, c, g, unknown or other FEATURE:
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LOCATION: (29)..(29)
OTHER INFORMATION: a, t,
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OTHER INFORMATION: a, t,
FEATURE:
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OTHER INFORMATION: a, t,
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OTHER INFORMATION: a, t,
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OTHER INFORMATION: a, t,
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OTHER INFORMATION: a, t,
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LOCATION: (201)..(1640)
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NAME/KEY: modified base
LOCATION: (578)..(579)
OTHER INFORMATION: a, t, c, g, unknown or other
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            c, g, unknown or other
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OTHER INFORMATION: a, t,
FEATURE:
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OTHER INFORMATION: a, t,
LOCATION: (429)
OTHER INFORMATION: a, t,
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LOCATION: (481)
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LOCATION: (605)
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NAME/KEY: modified base
LOCATION: (61)..(61)
OTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (75)..(75)
OTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (77)...(77)
OTHER INFORMATION: a, t, c, g, unknown or other
FEAPURE:
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LOCATION: (98)..(99)
OTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (95)..(96)
OTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (110)..(112)
OTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (120)..(\bar{1}20)
OTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (134)..(\bar{1}34)
OTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (143)..(143)
JTHER INFORMATION: a, t, c, g, unknown or other
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COCATION: (150)..(T50)
OTHER INFORMATION: a, t, c, g, unknown or other
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OTHER INFORMATION: a, t, c, g, unknown or other
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NAME/KEY: modified base
COCATION: (158)..(158)
FEATURE: INFORMATION: a, t, c, g, unknown or other
FEATURE:
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LOCATION: (182)..(182)
OTHER INFORMATION: a, t, c, g, unknown or other
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OTHER INFORMATION: a, t, c, g, unknown or other
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NAME/KEY: modified base
LOCATION: (155)..(156)
OTHER INFORMATION: a, t,
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                                                                                     NAME/KEY: modified base
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Query Match 6.5%; Score 87.6; DB 15; Length 1840;
Best Local Similarity 47.6%; Pred. No. 8.4e-11;
LOCATION: (186)...(186)
OTHER INFORMATION: a, t, c, g, unknown or other
                                                                  NAME/KEY: modified base
LOCATION: (189)..(189)
OTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (192)..(194)
OTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (224)..(227)
OTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (235)...(235)
OTHER INFORMATION: a, t, c, g, unknown or other
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NAME/KEY: modified base
OCCATION: (241)..(242)
OCHER INFORMATION: a, t, c, g, unknown or other
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NAME/KEY: modified base
LOCATION: (264)...(264)
OTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (270)..(369)
OTHER INFORMATION: a, t, c, g, unknown or other
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OTHER INFORMATION: a, t, c, g, unknown or other
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OTHER INFORMATION: a, t, c, g, unknown or other
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OTHER INFORMATION: a, L, C, g, unknown or other
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NAME/KEY: modified base
LOCATION: (506)..(506)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
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LOCATION: (528)..(528)
OTHER INFORMATION: a, t, c, g, unknown or other
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OTHER INFORMATION: a, t, c, g, unknown or other
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OTHER INFORMATION: a, t,
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LOCATION: (489)..(489)
OTHER INFORMATION: a, t,
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                                                          528 CGACCCGGAAGAAAAACCAAGAAGGCCACAGGCAGCCAAGGAAGCCGAGAAAGGGCC
                                                                                                 APPLICANT: Engelhard, Eric
APPLICANT: Engelhard, Eric
APPLICANT: Morris, David
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
FILE REFERENCE: A-70970/RMS/DCF
CURRENT APPLICATION NUMBER: US/10/004,113
CURRENT FILING DATE: 2001-10-23
PRIOR PILING DATE: 2001-10-23
PRIOR PLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2001-03-02
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 61
SOFTWARE: Patentin version 3.1
Indels
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 379;
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   Conservative
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US-10-004-113-43/c
   Matches 359;
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                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature; NAME/KEY: misc_feature; LOCATION: (39123)..(40764); COCATION: (39123)..(40764); OTHER INFORMATION: "n" at positions 39123 through 40764 can be any base.us-10-004-113-43
                                                                                                                                                                                                                         NAME/KEY: misc feature
LOCATION: (31054)..(31130)
OTHER INFORMATION: "n" at positions 31054 through 31130 can be any base.
                                                                                                                                                                                             LOCATION: (27928)..(28447)
OTHER INFORMATION: "n" at positions 27928 through 28447 can be any base.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16699 pagaalagaaagaagagagagagagagaaaagaaagaaggaaggaaggaaggaagaagaagaagaa
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LOCATION: (5939)..(6734)
OTHER INFORMATION: "n" at positions 5939 through 6734 can be any base.
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                                                                  any base
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                                                                                  NAME/KEY: misc feature
LOCATION: (3260)..(3314)
OTHER INFORMATION: "n" at positions 3260 through 3314 can be
                                                    LOCATION: (1302)..(1503)
OTHER INFORMATION: "n" at positions 1302 through 1503 can be
                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 288;
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Pred. No. 1e-09;
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                                                                                                                                                                                                                                                                                                                                               Query Match 6.2%;
Best Local Similarity 47.1%;
Matches 256; Conservative
                                                                                                                                                                                NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                   feature
TYPE: DNA
ORGANISM: Mus musculus
                                          NAME/KEY: misc feature
LOCATION: (1302)..(150
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APPLICANT: Sun, Yongwing
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Turner, Leah
TITLE OF INVENITON: Compositions and Methods Relating to Breast Specific Genes and
FILE REFERENCE: DEX-0267
CURRENT APPLICATION NUMBER: US/10/001, 843
CURRENT FILING DATE: 2001-11-20
PRIOR FILING DATE: 2000-11-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 80.6; DB 13;
Pred. No. 3.4e-09;
0; Mismatches 434;
                                                                                                                                                                 1316 CACACAGCAGAGAGAGAGA 1338
                                                                                                                                                                                               2571 AAAAATCAAAAAAAAAAAAA 2549
                                                                                                                                                                                                                                                                 Sequence 70, Application US/10001843; Publication No. US20020132255A1 GENERAL INFORMATION: APPLICANT: Salceda, Susana APPLICANT: Macina, Roberto
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Cafferkey, Robert
Sun, Yongming
Liu, Chenghua
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Best Local Similarity 46.2%;
Matches 379; Conservative (
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SOFTWARE: PatentIn version
SEQ ID NO 70
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APPLICANT:
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                                  APPLICATT: BERLIN. Kurt
TITLE OF INVENTION: Ortosine methylation
FILE OF INVENTION: Ortosine methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT APPLICATION NUMBER: DCT/EPO1/07537
PRIOR APPLICATION NUMBER: DCT/EPO1/07537
PRIOR APPLICATION NUMBER: DC 10032529.7
PRIOR PELING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PLING DATE: 2000-06-30
PRIOR PLING DATE: 2000-06-30
PRIOR PLING DATE: 2000-06-30
PRIOR SEQ ID NOS: 2424
SEQ ID NO 1670
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43.8%; Pred. No. 2.4e-09;
Live 0; Mismatches 451;
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              APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               al Similarity
352; Conserv
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US-10-311-455-1670
GENERAL INFORMATION:
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Best Local S.
Matches 352
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943 ACCGCGGAGGAAAGCCGAGACGAAAAGAAGGCAGGCGAAACGGGCGAACACAGAACA 1002
                                 886 AGGAGAAGAAGAAGGAAGGAGGCCAAGAAGAAAGGAAACGAAAGGAAAGTACAAACAGAA 945
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AG36550 Mus muscu
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Copyright (c) 1993 - 2004 Compugen Ltd.
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AG386733
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AG36153
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E Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.

E Direct Submission

Direct Submission

Submisted (17-NOV-203) Masahira Hattori, The Institute of Physical

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bp DNA linear GSS 03-JUN-2004
clone:MSMg01-305C02.TJ, genomic survey
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/mol type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"_____
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                 Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Droscphila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and BST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACC sesource Center can be found at http://bcpac.med.buffalo.edu/drosophila_bac.htm.
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                                                                                                                                                                                                                                                                                     /oxganism="Drosophila melanogaster"
/mol_type="qgnomic DNA"
/db_xref="taxon:7227"
/clone="BACR12K22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative 219; Mismatches 199;
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/note="end : TET3"
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and
                                               GAAGCCACAAAAAGACCACCCCCAAACACAGAGAGAAGGAGAACACACAGGAAGCCAAAG
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Ephydroidea; Drosophilidae; Drosophila.
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Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
Direct Submission
Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-311, Pars:81-45-503-9170
Clones are derived from the mouse BAC library MSNg01. For BAC
library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
Tsukuba Institude, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 dapan
phone: 81-208-36-9189, fax: 81-298-36-9199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AG386733 1189 bp DNA linear GSS 03-JUN-2004
Mus musculus molossinus DNA, clone:MSMg01-201A07.IJ, genomic survey
 1058 GGCAAAAGGGACCGAAAAAACCCCAGCCCACCCGAGAAGGAGACAGCCAAGCACAAAAAGGG 1117
                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                             Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
BAC end Sequences of Library MSMg01
Unpublished
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1. .1389
/organism="Mus musculus molossinus"
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/mol type="genomic DNA"
/mol species="molossinus"
/db xref="taxon:57486"
/clone="MSWG01-201A07.TJ"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            e-mail: abe@rtc.riken.jp
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AL Submitted (1-7007-203) Masahira Hattori, The Institute of Physical

and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

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(R-mail:hattoriegec.riken.jp, URL:http://hgp.gsc.riken.go.jp/,

Tel:81-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the mouse BAC library MSMg01. For BAC

library availability, please contact Kuniya Abe (abe@rtc.riken.jp).

Tsukuba Institute of Physical and Chemical Research (RIKEN) 3-1-1

Koyadai, Tsukuba, 305-0074 Japan

phone: 81-298-36-9189, fax: 81-298-36-9199

e-mail: abe@rtc.riken.jp

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Noguchi, H., Kojima, T. and Sakaki, Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h 8.7%; Score 117.4; DB 9; Length 1723; Similarity 45.6%; Pred. No. 1.4e-13; Observative 0; Mismatches 478; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue type="mixture of kidney and spleen'
/clone_lib="MSMg01 Mouse Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus molossinus"
/mol type="genomic DNA"
/sub_species="molossinus"
/db_xref="texon:57486"
/clone="MSMG01-305110.TJ"
                   Library MSMg01
                                                                                                                                                                                                                                                                                                                                                                               : ECOK1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                    : pBACe3.6
: EcoRI
    Toyoda, A.,
    Hattori,M., Toyoda,A.
BAC end Sequences of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sex="male"
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Mus musculus molossinus DNA, clone:MSMg01-146K01.TJ, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus molossinus
Mus musculus molossinus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                           651 AAGACCGAAGACCGCCAGAGCCCCAAAAGCCCAACAAGAAAGACACGGGACGAGGAAA
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                                                   Length 1389;
/tissue_type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"
                                                                         Indels
                                             Query Match
8.5%; Score 113.8; DB 9;
Best Local Similarity 47.9%; Pred. No. 7.4e-13;
Matches 360; Conservative 0; Mismatches 385;
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Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakakı,I.

Direct Submission
Submitted (17-NOY-2003) Masahira Hattori, The Institute of Physical
Submitted (17-NOY-2003) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-māl:hattori@geoc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
Clones are derived from the mouse BAC library MSMg01, For BAC
library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
Tsukuba Institute, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
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          Sakaki, Y.
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/clone_lib="MSMg01 Mouse Male BAC Library"
        Kojima, T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 113.8; DB 9; Length
Pred. No. 7.4e-13;
0; Mismatches 467; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'organism="Mus musculus molossinus"
                                                                                                                                                                                                                                                                                                                Koyadai, Tsukuba, 305-0074 Japan
phone: 81-296-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp
Hattori,M., Toyoda,A., Noguchi,H., BAC end Sequences of Library MSMg01
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic DNA"
/sub_species="molossinus"
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|clone="MSMg01-146K01,TJ"
|sex="male"
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Best Local Similarity 46.1%;
Matches 411; Conservative 0
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- Web : www.genoscope.cns.fr)

- Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACS. For further information please see http://www.fruifily.org The BDGP Drosophila melanogaster BAC library was prepared by Kazuctoyo Oscogawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial BCORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pi and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CNS00418 proposater genome survey sequence TET3 end of BAC #BACR09C16 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                         1048 ACCCAGGGGGGGGAAAAGGGACCGAAAAAACCCAGCCGAGAAGGAAGGAGACAGCCAAGC 1107
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GCAGAAAGGAAAGGCACCGCGGAAGGAAAGCCAGACAAGCCGAAAAGGAAGCAGGCGAAAACG
                                                                                                                                         Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
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/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fly), genomic survey sequence. ALO66537
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/clone lib="RPCI-98"
/note="end : TET3"
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2 (bases 1 to 1407)

Bitattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.

Bitattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.

Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

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Tel:81-45-503-911, Fax:81-45-503-9170)

Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp).

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The Institute of Physical and Chemical Research (RIKEN) 3-1-1

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phone: 81-298-36-9189, fax: 81-298-36-9199

e-mail: abe@rtc.riken.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1407 bp DNA linear GSS 02-JUN-2004
DNA, clone:MSMg01-141M24.T7, genomic survey
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Mus musculus molossinus
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Mammalia; Metazoa; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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Length 987;
Query Match

8.4%; Score 113.2; DB 9;
Best Local Similarity 27.5%; Pred. No. 9.5e-13;
Matches 147; Conservative 174; Mismatches 212;
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BAC end Sequences of Library MSMg01
Unpublished
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organism="Mus musculus molossinus"
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Pred. No. 2.1e-12;
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/sub_species="molossinus"
/db_xref="taxon:57486"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                  /tissue_type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"
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                                                                                   organism="Mus musculus molossinus"
                                                                                                                                                                                            8.4%; Score 112.8; DB 9;
45.9%; Pred. No. 1.2e-12;
live 0; Mismatches 536;
                                                                                             /mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
                                                                                                                            /clone="MSMg01-141M24.T7"
                                                               Location/Qualifiers
                              pBACe3.6
                                                                                                                                          /sex="male"
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         Sequencing: T7
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Vector: pBA(
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The Changes I to 1397)

All attorit, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
Direct Submission

Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mall:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
Clones are derived from the mouse BAC library MSMG01. For BAC
library avallability, please contect Kuniya Abe (abe@rtc.riken.jp).
Tsukuba Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
1247 GGAACGGACCGGACGACCCCAAACACCCAAGGAAACAGAAAAGCCCGCGGGCACG 1306
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                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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BAC end Sequences of Library MSMg01
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/clone_lib="MSMg01 Mouse Male BAC Library"
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Direct Submission

Direct Submission

Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou/Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSNgOI. For BAC
library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
Tsukuba Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 dapan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp
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Mus musculus molossinus
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                   Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
BAC end Sequences of Library MSMg01
Unpublished
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/clone_lib="MSMg01 Mouse Male BAC Library"
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46.3%; Pred. No. 2.5e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
/sub_species="molossinus"
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/clone="MSMg01-141B22.T7"
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  GI:47919388
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Hattori,M., Toyoda,A
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Mus musculus molossinus DNA, clone:MSMg01-141B22.T7, genomic survey
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        Indels
        Mismatches 485;
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         Conservative
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/lab_host="DH10B (phage-resistant)"
/clone lih="NIH MGC 100"
/note="Organ: līver; Vector: pOTB7; Site_1: XhoI; Site_2:
BCORI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
Library."
                                                                                                                                                                                                                                                                                                                    AGGAAGCGACCAAAAGAAAGCAACAGAAACGGCCCGACCAGCGGACCAACGAGAGCAGAA
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Pred. No. 3.2e-12;
0; Mismatches 554; Indels 19;
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602952764F1 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:5087103 5',
938 AAGGCACCGCGGAGGAAAGCCAGACAAGCCGAAAAGAAGCAGGCGAAACGAACACA
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/db_xref="taxon:9606"
/clone="IMAGE:5087103"
/tissue_type="hepatocellular carcinoma, cell line"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs.remail.nih.gov
Tissue Procurement: CGAP (Stanford)
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1843 row: p column: 16
High quality sequence stop: 73.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutel. Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo 1 (bases 1 to 1154)
MHH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
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                       ACAACCCGAAGGAGCACCAGCCAGGAGAACAGGAGAAGCACCGCGGGAGCAGAGAGAACAA
                                                                     AGAGACGCACACACACACAGGGCCCCCGGCGAAGCAGGAACCAGAAACCAGGGGCAGG
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Direct Submission
Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-tu, Yokohama, Kanagawa 230-0045, Japan
(E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSWg01. For BAC
library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
Tsukuba Institude, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
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                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
BAC end Sequences of Library MSMg01
Unpublished
                                                                                                                                        1243 CAAAGGAACGGACGGACGAGCCCCAAAACAGCAAGAAACAGAAAAAGCC
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43.8%; Pred. No. 4.8e-12;
tive 0; Mismatches 579;
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/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-141D13.T7"
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**Lobases to 1319)

15 2 (Dases to 1319)

16 Attori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.

Direct Submission

17 Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

17-72 Suehiro-chou,Taurumi-ku, Yokohama, Ranagawa 230-0045, Japan (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)

**Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp).

Tsukuba Institute of Physical and Chemical Research (RIKEN) 3-1-1

Koyadai, Tsukuba, 305-0074 Japan phone: 81-298-36-9189, fax: 81-298-36-9199
                                                                                                                                                                                                                                                1319 bp DNA linear GSS 02-JUN-2004 DNA, clone:MSMg01-111110.TJ, genomic survey
                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                            AAGCCAGACAAGCCGAAAAGAAGCAGGCGAAACGGGCGAACACAGAACAAAGAACGGCAG
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/tissue_type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"
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BAC end Sequences of Library MSMg01
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/sub_species="molossinus"
/db_xref="taxon:57486"
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S Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
Direct Submission

L Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
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Clones are derived from the mouse BAC library MSNg01. For BAC
library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
Tsukuba Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp
musculus molossinus DNA, clone:MSMg01-192K08.TJ, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1172 AGRANGARARAGAGAGAGAGARANGGAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAGA 1113
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       655 CCGAAGACCGCCAGAGCCCACAACCA-AGAAAGACACGGGACGAGGAAAAC 713
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BAC end Sequences of Library MSMg01
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|clone_lib="MSMg01 Mouse Male BAC Library"
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0; Mismatches 337; Indels
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/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-192K08.TJ"
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Best Local Similarity 49.5%; Pred. No. 6.
Matches 333; Conservative 0; Mismatche
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                             Gaps
                             19;
             Length 1319;
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             Score 108.4; DB 9;
Pred. No. 9.2e-12;
0; Mismatches 387;
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                     Best_Local Similarity 48.7
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Clones are derived from the mouse BAC library MSWG01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Trukuba Institude, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyagai, Tsukuba, 305-0074 Japan
Phone: 81-298-36-9189, fax: 81-298-36-9199
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                 Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
BAC end Sequences of Library MSMg01
Unpublished
                                                                                                                                                   Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
Direct Submission
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/clone_lib="mSMg01 Mouse Male BAC Library"
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llarity 45.4%; Pred. No. 1.4e-11;
Conservative 0; Mismatches 422;
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/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-161805.TJ"
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1044 AACAACCCAGGGGGGCAAAAAGGGACCGAAAAAACCCAGCCCACCCGAGAAGGAGACAGCC 1103
                          1104 AAGCACAAAAAGGGCAACAAAGGGGAAGGGCCAAAAGCACACCCCAACGAAAAGACAGGG 1163
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